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(54) **Non-reducing saccharide-forming enzyme, DNA encoding it, and their preparations and uses.**

(57) A DNA encoding an enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from amylaceous saccharides having a degree of glucose polymerization of 3 or higher, enables an industrial-scale production of a recombinant enzyme with such enzyme activity. Non-reducing saccharides obtainable by the recombinant enzyme can be used in a variety of food products, cosmetics, pharmaceuticals and feeds because of their substantial non-reducibility, mild and high-quality sweetness, adequate viscosity, and moisture-retaining ability.

EP 0 674 005 A2

The present invention relates to a novel DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and a recombinant DNA and enzyme containing the DNA as well as to a transformant. The present invention further relates to preparations and uses thereof.

Trehalose is a disaccharide which consists of 2 glucose molecules that are linked together with their reducing groups, and, naturally, it is present in fungi, algae, insects, etc., in an extremely small quantity. Having no reducing residue within the molecule, trehalose does not cause an unsatisfactory browning reaction even when heated in the presence of amino acids or the like, and because of this it can sweeten food products without fear of causing unsatisfiable coloration and deterioration. Trehalose, however, is far from being readily prepared in a desired amount by conventional production methods, and, actually, it has not scarcely been used for sweetening food products.

Conventional production methods are roughly classified into 2 groups, i.e. the one using cells of microorganisms and the other employing a multi-enzymatic system wherein enzymes are allowed to act on saccharides. The former, as disclosed in Japanese Patent Laid-Open No.154,485/75, is a method comprising growing microorganisms such as bacteria and yeasts in nutrient culture media, and collecting trehalose from the proliferated cells in the resultant cultures. The latter, as disclosed in Japanese Patent Laid-Open No.216,695/83, is a method comprising providing maltose as a substrate, allowing a multi-enzymatic system using maltose- and trehalose-phosphorylases to act on maltose, and recovering the formed trehalose from the reaction system. Although the former facilitates to grow microorganisms with a relative easiness, it requires sequential complicated steps for collecting trehalose from the microorganisms containing only 15 w/w % trehalose, on a dry solid basis (d.s.b.). While the latter enables to separate trehalose with a relative easiness, but it is theoretically difficult to increase the trehalose yield by allowing enzymes to act on substrates at a considerably-high concentration because the enzymatic reaction in itself is an equilibrium reaction of 2 different types of enzymes and the equilibrium point constantly inclines to the side of forming glucose phosphate.

In view of the foregoing, the present inventors energetically screened enzymes which form saccharides having trehalose structure from amylaceous saccharides, and found that microorganisms such as those of the spices *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 produce a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. Before or after this finding, it was revealed that such a non-reducing saccharide is almost quantitatively hydrolyzed into trehalose and glucose and/or maltooligosaccharides by another enzyme produced by the same microorganisms as mentioned above. Since the combination use of the enzymes enables to form a desired amount of trehalose with a relative easiness, the aforementioned objects relating to trehalose would be completely overcome. Insufficient producibility of the novel enzyme by such a microorganism results in a drawback, i.e. a relatively-large scale culture thereof is inevitable to industrially produce trehalose and/or non-reducing saccharides having trehalose structure as an end unit.

Recombinant DNA technology has made a remarkable progress in recent years. At present, even an enzyme whose total amino acid sequence has not been revealed can be readily prepared in a desired amount, if a gene encoding the enzyme was once isolated and the base sequence was decoded, by preparing a recombinant DNA which contains a DNA encoding the enzyme, introducing the recombinant DNA into microorganisms or cells of plants and animals, and culturing the resultant transformants. Under the background, urgently required are to find a gene encoding the enzyme and to reveal a base sequence thereof.

It is an aim of the present invention to provide a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

It is a further aim of the present invention to provide a recombinant DNA which contains the DNA and a self-replicable vector.

It is yet another aim of the present invention to provide a recombinant enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, by means of recombinant DNA technology.

It is another aim of the present invention to provide a transformant obtainable by introducing the recombinant DNA into a suitable host.

It is a further aim of the present invention to provide a preparation of the recombinant enzyme.

It is yet another aim of the present invention to provide a method to convert reducing amylaceous saccharides by using the recombinant enzyme.

The present invention provides a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

The present invention further provides a replicable recombinant DNA which contains a self-replicable vec-

tor and a DNA which encodes a non-reducing saccharide-forming enzyme.

The present invention further provides a recombinant enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

The present invention further provides a transformant into which a replicable recombinant DNA containing a self-replicable vector and a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

The present invention further provides a process for producing a recombinant enzyme, which contains a step of culturing a transformant capable of forming the recombinant enzyme, and collecting the enzyme from the resultant culture.

The present invention further provides a method for converting reducing amylaceous saccharides, which contains a step of allowing the recombinant enzyme to act on reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher to form from them non-reducing saccharides having trehalose structure as an end unit.

The invention will now be described in further detail, by way of example only, with reference to the accompanying drawings, in which:

FIG. 1 shows the optimum temperature of enzyme M-11.

FIG. 2 shows the optimum temperature of enzyme Q36.

FIG. 3 shows the optimum pH of enzyme M-11.

FIG. 4 shows the optimum pH of enzyme Q36.

FIG. 5 shows the thermal stability of enzyme M-11.

FIG. 6 shows the thermal stability of enzyme Q36.

FIG. 7 shows the pH stability of enzyme M-11.

FIG. 8 shows the pH stability of enzyme Q36.

FIG. 9 is a restriction map of the recombinant DNA pBMT7 according to the present invention. In the figure, a bold-lined part shows a DNA encoding enzyme M-11.

FIG. 10 is a restriction map of the recombinant DNA pBQT13 according to the present invention. In the figure, a bold-lined part shows a DNA encoding enzyme Q36.

The DNA according to the present invention exerts the production of the non-reducing saccharide-forming enzyme encoded by the DNA in a manner that the DNA is inserted into an appropriate self-replicable vector to form a replicable recombinant DNA, followed by introducing the recombinant DNA into a host, which is incapable of producing the enzyme but readily replicable, to form a transformant.

Although the recombinant DNA *per se* does not produce the enzyme, the production of the enzyme encoded by the DNA is induced by introducing the recombinant DNA into a host, which is incapable of producing the enzyme but replicable with a relative easiness, to form a transformant, and culturing the transformant to produce the enzyme.

The transformant according to the present invention produces the enzyme when cultured.

The recombinant enzyme according to the present invention acts on reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher to form non-reducing saccharides having trehalose structure as an end unit.

The culture of the transformant according to the present invention yields a desired amount of the enzyme with a relative easiness.

The conversion method according to the present invention converts reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher into non-reducing saccharides having trehalose structure as an end unit.

The present invention was made based on the finding of a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. The enzyme can be obtained from cultures of microorganisms of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 (the enzymes from *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 are respectively designated as "enzyme M-11" and "enzyme Q36" hereinafter), and the present inventors isolated the enzyme by the combination use of conventional purification methods using column chromatography mainly, and examined the properties and features to reveal the reality, i.e. a polypeptide having the following physicochemical properties:

(1) Action

Forming non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher;

(2) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE);
(3) Isoelectric point
About 3.6-4.6 on isoelectrophoresis;
(4) Optimum temperature
Exhibiting an optimum temperature of around 35-40°C when incubated at pH 7.0 for 60 min;
(5) Optimum pH
Exhibiting an optimum pH of around 6.4-7.2 when incubated at 40°C for 60 min;
(6) Thermal stability
Stable up to a temperature of around 35-40°C when incubated at pH 7.0 for 60 min; and
(7) pH Stability
Stable up to a pH of around 5.5-11.0 when incubated at 25°C for 16 hours.

The experiments, which were conducted to reveal the aforesaid physicochemical properties, are explained in the below:

Experiment 1

Preparation of purified enzyme

Experiment 1-1

Preparation of enzyme derived from *Rhizobium* sp. M-11

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) containing 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate, and 0.1 w/v % potassium dihydrogen phosphate, and the flasks were autoclaved at 120°C for 20 min to effect sterilization. After cooling the flasks a seed culture of *Rhizobium* sp. M-11 was inoculated into each liquid culture medium in each flask, followed by the incubation at 27°C for 24 hours under rotary-shaking conditions. Twenty L of a fresh preparation of the same liquid culture medium was put in a 30-L jar fermentor and sterilized, followed by inoculating one v/v % of the culture obtained in the above into the sterilized liquid culture medium in the jar fermentor, and incubating it at a pH of 6-8 and 30°C for 24 hours under aeration and agitation conditions.

Thereafter, about 18 L of the resultant culture was subjected to an ultra-high pressure cell disrupting apparatus to disrupt cells, and the resultant suspension was centrifuged to obtain a supernatant, and to about 16 L of which was added ammonium sulfate to give a 20 w/v % saturation, allowed to stand at 4°C for one hour, and centrifuged to remove sediment. To the resultant supernatant was added ammonium sulfate to give a 60 w/v % saturation, allowed to stand at 4°C for 24 hours, and centrifuged to collect sediment which was then dissolved in a minimum amount of 10 mM phosphate buffer (pH 7.0). The resultant solution was dialyzed against 10 mM phosphate buffer (pH 7.0) for 24 hours, and centrifuged to remove insoluble substances. The supernatant thus obtained was fed to a column packed with "DEAE-TOYOPEARL®", a product for ion-exchange chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM phosphate buffer (pH 7.0), followed by feeding to the column a linear gradient buffer of sodium chloride ranging from 0 M to 0.5 M in 10 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, dialyzed for 10 hours against 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, and centrifuged to remove insoluble substances. Thereafter, the resultant supernatant was fed to a column, which had been packed with "BUTYL TOYOPEARL®", a gel for hydrophobic column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, and equilibrated with 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, followed by feeding to the column a linear gradient buffer of ammonium sulfate ranging from 2 M to 0 M in 50 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, fed to a column packed with "TOYOPEARL® HW-55", a product for gel filtration column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 50 mM phosphate buffer (pH 7.0), followed by feeding to the column 50 mM phosphate buffer (pH 7.0) and collecting fractions containing the objective enzyme. The enzyme thus obtained had a specific activity of about 195 units/mg protein, and the yield was about 220 units per L of the culture.

Throughout the specification the enzyme activity is expressed by the value measured on the following assay: Place 4 ml of 50 mM phosphate buffer (pH 7.0) containing 1.25 w/v % maltopentaose in a test tube, add one ml of an enzyme solution to the tube, and incubate the resultant solution at 40°C for 60 min to effect enzymatic reaction. Thereafter, heat the resultant reaction mixture at 100°C for 10 min to suspend the enzymatic reaction. Dilute the resultant reaction mixture with distilled water by 10 times, and assay the reducing activity

on the Somogyi-Nelson's method. One unit activity of the enzyme is defined as the amount of enzyme which reduces the reducing power corresponding to one μmol maltopentaose per min under the same conditions as described above.

Experiment 1-2

Purification of enzyme Q36

Similarly as in Experiment 1-1, a seed culture of *Arthrobacter* sp.Q36 was cultured, and the resultant culture was treated to obtain a purified enzyme Q36 having a specific activity of about 200 units/mg protein in a yield of about 295 units per L of the culture.

Experiment 2

Physicochemical property of enzyme

Experiment 2-1

Action

To 50 mM phosphate buffer (pH 7.0) containing 20 w/v % of glucose, maltose, maltotriose, maltotetraose, maltopentaose, maltohexaose or maltoheptaose as a substrate was added 2 units/g substrate, d.s.b., of the purified enzyme M-11 or enzyme Q36 obtained in Experiment 1, and the mixture was enzymatically reacted at 40°C for 48 hours. The reaction mixture was desalted in usual manner, fed to "WB-T-330", a column for high-performance liquid chromatography (HPLC) commercialized by Tosoh Corporation, Tokyo, Japan, followed by feeding to the column distilled water at a flow rate of 0.5 ml/min at ambient temperature to separate saccharides contained in the reaction mixture while monitoring the saccharide concentration of the eluate with "MODEL RI-8012", a differential refractometer commercialized by Wako Pure Chemical Industries, Ltd., Tokyo, Japan. The saccharide composition of the reaction mixture was given in Table 1 or 2. In the table, the symbols "*P1*" to "*P5*" were named for the formed saccharides in the order from the smallest one to the largest one in terms of their degrees of glucose polymerization.

Table 1

Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Glucose	Glucose	33.4	100.0
Maltose	Maltose	28.5	100.0
Maltotriose	P1	23.3	35.0
	+ Maltotriose	25.9	65.0
Maltotetraose	P2	21.6	85.6
	+ Maltotetraose	24.1	14.4
Maltopentaose	P3	19.7	92.7
	+ Maltopentaose	22.6	7.3
Maltohexaose	p4	18.7	93.5
	+ Maltohexaose	21.4	6.5
Maltoheptaose	P5	17.8	93.4
	+ Maltoheptaose	21.0	6.7

Table 2

Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Glucose	Glucose	33.4	100.0
Maltose	Maltose	28.5	100.0
Maltotriose	P1 + Maltotriose	23.3 25.9	35.5 64.5
Maltotetraose	P2 + Maltotetraose	21.6 24.1	85.8 14.2

(Continued)

Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Maltopentaose	P3 + Maltopentaose	19.7 22.6	92.9 7.1
Maltohexaose	P4 + Maltohexaose	18.7 21.4	93.2 6.7
Maltoheptaose	P5 + Maltoheptaose	17.8 21.0	93.1 6.9

As is evident from the results in Table 1 and 2, the enzymes M-11 and Q36 newly formed saccharides from reducing saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose, but not from those having a degree of glucose polymerization less than 3 such as glucose and maltose. In the enzymatic reaction, the newly formed saccharides were **P1** to **P5**, and the total yield of the saccharides **P2** to **P5** was as high as 85 w/w % or more, d.s.b.

To separate the saccharides **P1** to **P5**, 3 jacketed stainless steel columns, having an inner diameter of 2.0 cm and a length of one m, were packed with "XT-1016, Na^{+}", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series. The reaction mixture containing any one of saccharides **P1** to **P5** was separatory applied to the columns at an inner column temperature of 55°C, followed by applying to the columns with 55°C distilled water at a flow rate of SV (space velocity) 0.13. After examining the saccharide composition of the resultant eluate, a fraction containing 97 w/w or more, d.s.b., of any one of saccharides **P1** to **P5** was recovered and pulverized in vacuo. No substantial reducing power was detected in the purified saccharides **P1** to **P5** on the Somogyi-Nelson's method.

To identify the saccharides P1 to P5, 50 mg one of which was weighed, dissolved in one ml of 50 mM acetate buffer (pH 4.5), and mixed with one unit of glucoamylase, followed by incubating the mixture at 40°C for 6 hours. High-performance liquid chromatography analysis on the resultant reaction mixture detected glucose and trehalose as shown in Tables 3 and 4. When the saccharides **P1** to **P5** were subjected to the action of β-amylase, the saccharides **P1** and **P2** were not hydrolyzed by β-amylase, but the saccharides **P3**, **P4** and **P5** were respectively hydrolyzed into one mole of maltose, **P2** and one mole of maltose, and **P1** and 2 moles of maltose.

Table 3

Substrate	Glucose (%)	Trehalose (%)	Molar ratio*
P1	36.2	63.8	1.07
P2	52.0	48.0	2.06
P3	61.4	38.6	3.02
P4	68.3	31.7	4.09
P5	72.9	27.1	5.11

Note: The molar ratios as indicated with the symbol "*" are values calculated as moles of glucose against one mole of trehalose.

Table 4

Substrate	Glucose (%)	Trehalose (%)	Molar ratio*
P1	36.0	64.0	1.07
P2	51.5	48.5	2.02
P3	61.6	38.4	3.05
P4	68.1	31.9	4.06
P5	72.5	27.5	5.01

Note: The molar ratios as indicated with the symbol "*" are values calculated as moles of glucose against one mole of trehalose.

The results in Tables 3 and 4 strongly show that the saccharides **P1** to **P5** consist of one mole of trehalose and 1 to 5 moles of glucose. From the facts that glucoamylase specifically hydrolyzes the α-1,4 and α-1,6 linkages in maltooligosaccharides and that β-amylase hydrolyzes the a-1,4 linkage in maltooligosaccharides from their end terminals by maltose units, it is estimated that the saccharides **P1** to **P5** have a structure consisting of glucose or maltooligosaccharide having a degree of glucose polymerization of 2 to 5, both of which have a trehalose residue at their end terminals.

The total judgement of the above results identifies the saccharides **P1** to **P5** as a-glucosyl trehalose, α-maltosyl trehalose, α-maltotriosyl trehalose, a-maltotetraosyl trehalose and α-maltopentaosyl trehalose respectively, and this evidences that the enzymes have an activity of forming non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher.

Experiment 2-2

Molecular weight

In accordance with the method reported by U. K. Laemmli in *Nature*, Vol.227, pp.680-685 (1970), the purified enzymes M-11 and Q36 in Experiment 1 were respectively electrophoresed on sodium dodecyl polyacrylamide gel electrophoresis to give a single protein band at a position corresponding to about 76,000-87,000 daltons. The marker proteins used in this experiment were myosin (MW=200,000 daltons), β-galactosidase (MW=116,250 daltons), phosphorylase B (MW=97,400 daltons), serum albumin (MW=66,200 daltons) and ovalbumin (MW=45,000 daltons).

Experiment 2-3

Isoelectric point

The purified enzymes M-11 and Q36 obtained in Experiment 1 gave an isoelectric point of about 3.6-4.6 on isoelectrophoresis respectively.

Experiment 2-4

Optimum temperature

The optimum temperature of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 35-40°C as shown in FIG. 1 or 2 when incubated in usual manner in 50 mM phosphate buffer (pH 7.0) for 60 min.

Experiment 2-5

Optimum pH

The optimum pH of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 6.4-7.2 as shown in FIG. 3 or 4 when experimented in usual manner by incubating them at 40°C for 60 min in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

Experiment 2-6

Thermal stability

The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a temperature of about 35-40°C as shown in FIGs. 5 and 6 when experimented in usual manner by incubating them in 50 mM phosphate buffer (pH 7.0) for 60 min.

Experiment 2-7

pH Stability

The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a pH of about 5.5-11.0 as shown in FIGs. 7 and 8 when experimented in usual manner by incubating them at 25°C for 16 hours in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

Experiment 2-8

Amino acid sequence containing the N-terminal

The amino acid sequence containing the N-terminal of the purified enzyme M-11 obtained in Experiment 1 was analyzed on "MODEL 470 A", a gas-phase protein sequencer commercialized by Applied Biosystems, Inc., Foster City, USA, to reveal that enzyme M-11 has an amino acid sequence as shown in SEQ ID NO:12.

The amino acid sequence containing the N-terminal of the purified enzyme Q36 was analyzed similarly

as in enzyme M-11 to reveal that it has an amino acid sequence as shown in SEQ ID NO:13.

Experiment 2-9

Partial amino acid sequence

An adequate amount of the purified enzyme M-11 obtained in Experiment 1-1 was weighed, dialyzed against 10 mM Tris-HCl buffer (pH 9.0) at 4°C for 18 hours, and admixed with 10 mM Tris-HCl buffer (pH 9.0) to give a concentration of about one mg/ml of the enzyme. About one ml of the resultant solution was placed in a container, admixed with 10 µg lysyl endopeptidase, and incubated at 30°C for 22 hours to partially hydrolyze the enzyme. The resultant hydrolysate was applied to "CAPCELL-PAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Shiseido Co., Ltd., Tokyo, Japan, which had been previously equilibrated with 0.1 v/v % trifluoroacetate containing 16 v/v % aqueous acetonitrile, followed by feeding to the column 0.1 v/v % trifluoroacetate at a flow rate of 0.9 ml/min while increasing the concentration of acetonitrile from 16 to 64 v/v % to separatory collect fractions containing a peptide fragment about 28 min or 40 min after the initiation of feeding (the peptide fragments were respectively named "peptide fragment **A**" and "peptide fragment **B**"). Fractions containing the peptide fragment **A** or **B** were separatory pooled, dried *in vacuo*, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Similarly as in Experiment 2-8, the peptide fragments A and B were analyzed and revealed to have an amino acid sequence as shown in SEQ ID NO:14 and an amino acid sequence as shown in SEQ ID NO:15.

Similarly as in enzyme M-11, enzyme Q36 obtained in Experiment 1-2 was partially hydrolyzed, and the resultant was fed to "µBONDAPAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Japan Millipore Ltd., Tokyo, Japan, followed by feeding to the column 0.1 v/v % trifluoroacetate containing aqueous acetonitrile raging from a concentration of 24 v/v % to 44 v/v % at a flow rate of 0.9 ml/ml. Fractions containing a peptide fragment eluted about 22 min or about 40 min after the initiation of feeding (the fractions were respectively called "peptide fragment **C**" and "peptide fragment **D**" hereinafter) were respectively collected, pooled, dried *in vacuo*, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Analyses of the peptide fragments **C** and **D** conducted similarly as above revealed that they have amino acid sequences as shown in SEQ ID NOs:16 and 17, respectively.

No enzyme having these physicochemical properties has been known, and this concluded that it is a novel substance. Referring to *Rhizobium* sp. M-11, it is a microorganism which was isolated from a soil of Okayama-city, Okayama, Japan, deposited on December 24, 1992, in National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology, Tsukuba, Ibaraki, Japan, and accepted under the accession number of FERM BP-4130, and it has been maintained by the institute. *Arthrobacter* sp. Q36 is a microorganism which was isolated from a soil of Soja-city, Okayama, Japan, deposited on June 3, 1993, in the same institute, and accepted under the accession number of FERM BP-4316, and it has been maintained by the institute. Japanese Patent Application No.349,216/93 applied by the same applicant discloses the properties and features of the non-reducing saccharide-forming enzyme as well as the detailed bacteriological properties of these microorganisms.

The present inventors energetically screened a chromosomal DNA of *Rhizobium* sp. M-11 by using an oligonucleotide as a probe which had been chemically synthesized based on the partial amino acid sequence of enzyme M-11 as revealed in Experiment 2-9, and found a DNA fragment which consists of 2,316 base pairs having a base sequence as shown in the following SEQ ID NO:1 which initiates from the 5'-terminus. The decoding of the base sequence revealed that the enzyme consists of 772 amino acids as shown in SEQ ID NO:2.

Similarly as in enzyme M-11, a chromosomal DNA of enzyme Q36 was screened by using an oligonucleotide as a probe which had been chemically synthesized based on a partial amino acid sequence of enzyme Q36, and this yielded a DNA fragment having a base sequence consisting of 2,325 base pairs from the 5'-terminus as shown in SEQ ID NO:3. The base sequence was decoded to reveal that enzyme Q36 consists of 775 amino acids and has a partial amino acid sequence containing the N-terminal as shown in SEQ ID NO:4.

The sequential experimental steps used to reveal the base sequence and amino acid sequence as shown in SEQ ID NOs:1 to 4 are summarized as below:

(1) The enzyme was isolated from a culture of a donor microorganism and highly purified. The purified enzyme was partially hydrolyzed with protease, and the resultant 2 different types of peptide fragments were isolated and determined their amino acid sequences;

(2) Separately, a chromosomal DNA was isolated from a donor microorganism's cell, purified and partially digested by a restriction enzyme to obtain a DNA fragment consisting of about 3,000-7,000 base pairs. The DNA fragment was ligated by DNA ligase to a plasmid vector, which had been previously cut with a restriction enzyme, to obtain a recombinant DNA;

(3) The recombinant DNA was introduced into *Escherichia coli* to obtain transformants, and from which an objective transformant containing a DNA encoding the enzyme was selected by the colony hybridization method using as a probe an oligonucleotide which had been chemically synthesized based on the aforesaid partial amino acid sequence; and

(4) The recombinant DNA was obtained from the transformant and annealed with a primer, followed by allowing a DNA polymerase to act on the resultant to extend the primer, and determining the base sequence of the resultant complementary chain DNA by the dideoxy chain termination method. The comparison of an amino acid sequence estimable from the determined base sequence with the aforesaid amino acid sequence confirmed that the base sequence encodes the enzyme.

As is explained in the above, the enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, is an enzyme which was found as a result of the present inventors' long-term research. The enzyme has distinct physicochemical properties from those of other conventional enzymes. The present invention is to produce the enzyme by applying recombinant DNA technology. The recombinant DNA, and its preparation and uses are explained in detail with reference to examples.

The recombinant enzyme as referred to in the invention means the whole enzymes which are preparable by recombinant DNA technology and capable of forming non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. Generally, the recombinant enzyme according to the present invention has a revealed amino acid sequence, and, as an example, the amino acid sequence, which initiates from the N-terminal as shown in SEQ ID NO:2 or 4, and homologous ones to it can be mentioned. Variants having amino acid sequences homologous to the one as shown in SEQ ID NO:2 or 4 can be obtained by replacing one or more bases in SEQ ID NO:2 or 4 with other bases without substantially alternating the inherent action of the enzyme. Although even when used the same DNA and it also depends on hosts into which the DNA is introduced, ingredients and components of nutrient culture media for culturing transformants, and their cultivation temperature and pH, there may be produced modified enzymes which have amino acid sequences similar to that of SEQ ID NO:2 or 4 as well as having an enzymatic action of the enzyme encoded by the DNA but defecting one or more amino acids located nearness to the N-terminal of the amino acid sequence as shown in SEQ ID NO:2 or 4 and/or having one or more amino acids newly added after the DNA expression to the N-terminal by the modification of intracellular enzymes of hosts. The recombinant enzyme can be obtained from cultures of transformants containing a specific DNA. Examples of such a transformant used in the invention can be prepared by introducing into hosts a DNA having either the base sequence which initiates from the N-terminal or a homologous base sequence to it or a complementary base sequence to them. Such a base sequence may be prepared by replacing one or more bases thereof without alternating the amino acid sequence encoded thereby by using degeneracy of genetic code. Needless to say, one or more bases in the base sequence, which encodes the enzyme or their variants, can be readily replaced with other bases to allow the DNA to actually express the enzyme production in hosts.

The DNA usable in the present invention includes any one of those derived from natural resources and artificially synthesized ones as long as they have such an aforementioned base sequence. The natural resources for the DNA according to the present invention are, for example, microorganisms of the genera *Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium* and *Terrabacter,* i.e. *Rhizobium* sp. M-11 (FERM BP-4130), *Arthrobacter* sp. Q36 (FERM BP-4316), *Brevibacterium helovolum* (ATCC 11822), *Flavobacterium aquatile* (IFO 3772), *Micrococcus luteus* (IFO 3064), *Micrococcus roseus* (ATCC 186), *Curtobacterium citreum* (IFO 15231), *Mycobacterium smegmatis* (ATCC 19420) and *Terrabacter tumescens* (IFO 12960) from which genes containing the present DNA can be obtained. The aforementioned microorganisms can be inoculated in nutrient culture media and cultured for about 1-3 days under aerobic conditions, and the resultant cells were collected from the cultures and subjected to ultrasonication or treated with a cell-wall lysis enzyme such as lysozyme or β-glucanase to extract genes containing the present DNA. In this case, a proteolytic enzyme such as protease can be used along with the cell-wall lysis enzyme, and, in the case of treating the cells with an ultrasonic disintegrator, they may be treated in the presence of a surfactant such as sodium dodecyl sulfate (SDS) or may be treated with freezing and thawing. The objective DNA is obtainable by treating the resultant with phenol extraction, alcohol sedimentation, centrifugation, protease treatment and/or ribonuclease treatment used in general in this field. To artificially synthesize the present DNA, it can be chemically synthesized by using the base sequence as shown in SEQ ID NO:1 or 3, or can be obtained in a plasmid form by inserting a DNA which encodes the amino acid sequence as shown in SEQ ID NO:2 or 4 into an appropriate self-replicable vector to obtain a recombinant DNA, introducing the recombinant DNA into an appropriate host to obtain a transformant, culturing the transformant, separating the proliferated cells from the resultant culture, and collecting plasmids containing the DNA from the cells.

Such a recombinant DNA is generally introduced into hosts in a recombinant DNA form. Generally, the recombinant DNA contains the aforesaid DNA and a self-replicable vector, and it can be prepared with a relative easiness by recombinant DNA technology in general when the material DNA is in hand. Examples of such a vector are plasmid vectors such as pBR322, pUC18, Bluescript II SK(+), pUB110, pTZ4, pC194, pHV14, TRp7, TEp7, pBS7, etc.; and phage vectors such as λgt·λC, λgt·λB, ρ11, φ1, φ105, etc. Among these plasmid- and phage-vectors, pBR322, pUC18, Bluescript II SK(+), λgt·λC and λgt·λB are satisfactorily used when the present DNA needs to be expressed in *Escherichia coli*, while pUB110, pTZ4, pC194, ρ11, φ1 and φ105 are satisfactorily used to express the DNA in microorganisms of the genus *Bacillus*. The plasmid vectors pHV14, TRp7, TEp7 and pBS7 are advantageously used when the recombinant DNA is allowed to grow in 2 or more hosts.

The methods used to insert the present DNA into such a vector in the invention may be conventional ones in general in this field. A gene containing the present DNA and a self-replicable vector are first digested by a restriction enzyme and/or ultrasonic disintegrator, then the resultant DNA fragments and vector fragments are ligated. To digest DNAs and vectors, restriction enzymes which specifically act on nucleotides, particularly, type II restriction enzymes, more particularly *Sau* 3AI, *Eco* RI, *Hind* III, *Bam* HI, *Sal* I, *Xba* I, *Sac* I, *Pst* I, etc., facilitate the ligation of the DNA fragments and vector fragments. To ligate the DNA fragments with vector fragments, they are annealed if necessary, then subjected to the action of a DNA ligase in vivo or in vitro. The recombinant DNA thus obtained is replicable without substantial limitation by introducing it into appropriate hosts, and culturing the resultant transformants.

The recombinant DNA thus obtained can be introduced into appropriate host microorganisms including *Escherichia coli* and those of the genus *Bacillus* as well as actinomyces and yeasts. In the case of using *Escherichia coli* as a host, the DNA can be introduced thereinto by culturing the host in the presence of the recombinant DNA and calcium ion, while in the case of using a microorganism of the genus *Bacillus* as a host the competent cell method and the colony hybridization method can be employed. Desired transformants can be cloned by the colony hybridization method or by culturing a variety of transformants in nutrient culture media containing reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and selecting the objective transformants which form non-reducing amylaceous saccharides having trehalose structure as an end unit from the reducing amylaceous saccharides.

The transformants thus obtained extracellularly produce the objective enzyme when cultured in nutrient culture media. Generally, liquid culture media in general supplemented with carbon sources, nitrogen sources and minerals, and, if necessary, further supplemented with small amounts of amino acids and vitamins can be used in the invention. Examples of the carbon sources are saccharides such as starch, starch hydrolysate, glucose, fructose and sucrose. Examples of the nitrogen sources are organic- and inorganic-substances containing nitrogen such as ammonia, ammonium salts, urea, nitrate, peptone, yeast extract, defatted soy been, corn steep liquor, and beef extract. Cultures containing the objective enzyme can be prepared by inoculating the transformants into nutrient culture media, and incubating them at a temperature of 25-65°C and a pH of 2-8 for about 1-6 days under aerobic conditions by aeration and agitation. Such a culture can be used intact as an enzyme agent, and, usually, it may be disrupted prior to use with ultrasonic disintegrator and/or cell-wall lysis enzymes, followed by separating the enzyme from the intact cells and cell debris by filtration and/or centrifugation and purifying the enzyme. The methods to purify the enzyme include conventional ones in general. From cultures intact cells and cell debris are eliminated and subjected to one or more methods such as concentration, salting out, dialysis, separatory sedimentation, gel filtration chromatography, ionexchange chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectric point electrophoresis.

As is described above, the recombinant enzyme according to the present invention has a specific feature of forming non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. The formed non-reducing saccharides have a satisfactorily mild and high-quality sweetness as well as an adequate viscosity and moisture-retaining ability, and, as a great advantageous feature, they can sweeten food products without fear of causing coloration and deterioration because they do not have a reducing residue within their molecule. By using these features a variety of amylaceous saccharides, which have been put aside because of their reducibilities, can be converted into saccharides having a satisfactory handleability and usefulness but having substantially no or extremely-reduced reducibility.

Now explaining the conversion method in more detail, reducing starch hydrolysates, which are obtainable by partially hydrolyzing amylaceous saccharides such as starch, amylopectin and amylose by acids and/or amylases, can be usually used as the substrate for the present recombinant enzyme. Such a starch hydrolysate can be obtained by conventional methods in general used in the art, and examples thereof include one or more maltooligosaccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose. As described in "*Handbook of Amylases and Re-*

lated Enzymes", 1st edition, edited by The Amylase Research Society of Japan, published by Pergamon Press plc, Oxford, England (1988), α-amylase, maltotetraose-forming amylase, maltopentaose-forming amylase and maltohexaose-forming amylase are especially useful to prepare the reducing amylaceous saccharides used in the invention, and, the use of any one of these amylases readily yields amylaceous saccharide mixtures rich in reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher in a considerably-high yield. If necessary, the combination use of the amylases and starch debranching enzymes such as pullulanase and isoamylase can increase the yield of the reducing amylaceous saccharides used as the substrate for the present recombinant enzyme.

In the conversion method according to the present invention, the present recombinant enzyme is allowed to coexist in an aqueous solution containing one or more of the aforesaid reducing amylaceous saccharides as a substrate, and allowing the solution to enzymatically react at a prescribed temperature and pH until a desired amount of the objective reducing amylaceous saccharides is formed. Although the enzymatic reaction proceeds even below a concentration of 0.1 w/v % of a substrate, a higher concentration of 2 w/v %, preferably, 5-50 w/v % of a substrate can be satisfactorily used to apply the present conversion method to an industrial-scale production. The temperature and pH used in the enzymatic reaction are set within the ranges of which do not inactivate the recombinant enzyme and allow the recombinant enzyme to effectively act on substrates, i.e. a temperature up to about 55°C, preferably, a temperature in the range of about 40-55°C, and a pH of 5-10, preferably, a pH in the range of about 6-8. The amount and reaction time of the present recombinant enzyme are chosen dependently on the enzymatic reaction condition. The enzymatic reaction relatively-highly reduces the reducing power of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and, in the case of maltopentaose, the reducing powder is lowered to about 7% against the original level.

The reaction mixtures obtained by the present conversion reaction can be used intact, and, usually, they are purified prior to use: Insoluble substances are eliminated from the reaction mixtures by filtration and centrifugation, and the resultant solutions are decolored with an activated charcoal, desalted and purified on ion exchangers, and concentrated into syrupy products. Dependently on their use, the syrupy products are dried *in vacuo* and spray-dried into solid products. In order to obtain products which substantially consist of non-reducing saccharides, the aforesaid syrupy products are subjected to one or more methods such as chromatography using an ion exchanger, activated charcoal and silica gel for saccharide separation, separatory sedimentation using alcohol and/or acetone, membrane filtration, fermentation by yeasts, and removal and decomposition of reducing saccharides by alkalis. The methods to treat a large amount of reaction mixture are, for example, fixed bed- or pseudomoving bed-ion exchange column chromatography as disclosed in Japanese Patent Laid-Open Nos.23,799/83 and 72,598/83, and such a method produces non-reducing saccharide-rich products in an industrial scale and in a considerably-high yield.

The reducing saccharides thus obtained have a wide applicability to a variety of products which are apt to be readily damaged by the reducibility of saccharide sweeteners: For example, they can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. Since the non-reducing saccharides approximately qualitatively form trehalose when received an enzymatic action of a trehalose-releasing enzyme as disclosed in Japanese Patent Application No.340,343/93, they can be used as an intermediate for the production of trehalose which could not have been readily prepared.

The following examples explain the present invention in more detail, and the recombinant DNA technologies or techniques employed therein are in themselves conventional ones used in the art, for example, those described by J. Sumbruck et al. in "*Molecular Cloning A Laboratory Manual*", 2nd edition, published by Cold Spring Harbor Laboratory Press, USA (1989).

Example 1

Preparation of recombinant DNA containing DNA derived from enzyme M-11, and transformant

Example 1-1

Preparation of chromosomal DNA

A seed culture of *Rhizobium* sp. M-11 was inoculated into bacto nutrient broth medium (pH 7.0), and cultured at 27°C for 24 hours with a rotary shaker. The cells were separated from the resultant culture by centrifugation, suspended in TES buffer (pH 8.0), admixed with 0.05 w/v % lysozyme, and incubated at 37°C for 30 min. The resultant was freezed at -80°C for one hour, admixed with TSS buffer (pH 9.0), heated to 60°C, and admixed with a mixture solution of TES buffer and phenol, and the resultant solution was chilled with ice, fol-

lowed by centrifugally collecting the precipitated crude chromosomal DNA. To the supernatant was added 2 fold volumes of cold ethanol, and the precipitated crude chromosomal DNA was collected, suspended in SSC buffer (pH 7.1), admixed with 7.5 μg ribonuclease and 125 μg protease, and incubated at 37°C for one hour. Thereafter, a mixture solution of chloroform and isoamyl alcohol was added to the reaction mixture to extract the objective chromosomal DNA, and admixed with cold ethanol, followed by collecting the formed sediment containing the chromosomal DNA. The purified chromosomal DNA thus obtained was dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the solution was freezed at -80°C.

Example 1-2

Preparation of recombinant DNA pBMT7 and transformant BMT7

About one ml of the purified chromosomal DNA obtained in Example 1-1 was placed in a container, admixed with about 35 units of *Sau* 3AI, a restriction enzyme, and enzymatically reacted at 37°C for about 20 min to partially digest the chromosomal DNA, followed by recovering a DNA fragment consisting of about 3,000-7,000 base pairs by sucrose density-gradient ultracentrifugation. One μg of Bluescript II SK(+), a plasmid vector, was provided, subjected to the action of *Bam* HI, a restriction enzyme, to completely digest the plasmid vector, admixed with 10 μg of the DNA fragment and 2 units of T4 DNA ligase, and allowed to stand at 4°C overnight to ligate the DNA fragment to the vector fragment. To the resultant recombinant DNA was added 30 μl of "Epicurian Coli® XLI-Blue", competent cell commercialized by Toyobo Co., Ltd., Tokyo, Japan, allowed to stand under ice-chilled conditions for 30 min, heated to 42°C admixed with SOC broth, incubated at 37°C for one hour to introduce the recombinant DNA into *Escherichia coli.*

The resultant transformant was inoculated into agar plate (pH 7.0) containing 50 μg/ml of 5-bromo-4-chloro-3-indolyl-β-galactoside, and cultured at 37°C for 18 hours, followed by placing a nylon film on the agar plate to fix thereon about 4,400 colonies formed on the agar plate. Based on the amino acid sequence of Pro-Glu-Trp-Glu-Lys located at positions from 17 to 21 in the amino acid sequence of the peptide fragment **A** as revealed in Experiment 2-9, the base sequence of probe 1 as shown in SEQ ID NO:5 was chemically synthesized, labelled with ^{32}P, and hybridized with the colonies of transformants fixed on the nylon film, followed by selecting 9 transformants which exhibited a strong hybridization.

The objective recombinant DNA was selected in usual manner from the 9 transformants, and, in accordance with the method described by E. M. Southern in *Journal of Molecular Biology*, Vol.98, pp.503-517 (1975), hybridized with probe **2** having the base sequence as shown in SEQ ID NO:6 which had been chemically synthesized based on the amino acid sequence of Thr-Glu-Phe-Trp-Asp located at positions from 16 to 20 in the amino acid sequence of the peptide fragment **B** as revealed in Experiment 2-9 , followed by selecting a recombinant DNA which strongly hybridized with probe **2**. The recombinant DNA and transformant thus selected were respectively named pBMT7 and BMT7.

The transformant BMT7 obtained in the above was inoculated into L-broth (pH 7.0) containing 100 μg/ml ampicillin, and cultured at 37°C for 24 hours with a rotary shaker. After completion of the culture, the cells were collected from the culture by centrifugation, and treated with the alkaline method in general to extracellularly extract a recombinant DNA. The resultant was in usual manner purified and analyzed to find that the recombinant DNA pBMT7 consists of about 9,300 base pairs and has a structure expressed by the restriction map as shown in FIG. 9. It was revealed that as shown in FIG. 9 the DNA consisting of 2,316 base pairs encoding enzyme M-11 is located in the downstream near to the digested site by *Pst* I, a restriction enzyme.

Example 1-3

Production of enzyme by transformant

A liquid medium consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50 μg/ml ampicillin, autoclaved at 120°C for 20 min, cooled and inoculated with a seed culture of transformant BMT7 obtained in Example 1-2, followed by culturing the transformant at 37°C for 24 hours with a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 3,000 units of the enzyme.

As a control, a seed culture of *Escherichia coli* XLI-Blue or *Rhizobium* sp. M-11 was inoculated into a fresh preparation of the same liquid culture medium but free of ampicillin, and, in the case of the culture of *Rhizobium* sp. M-11, it was cultured and treated similarly as above except that the culturing temperature was set to 30°C.

Assaying the resultant activity, one L culture of *Rhizobium* sp. M-11 yielded about 1,500 units of the enzyme, and the yield was significantly lower than that of transformant BMT7. *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BMT7 purified similarly as in Experiment 1-1, and examined on the properties and characteristics. As a result, it was revealed that it has substantially the same physicochemical properties as that of Experiment 2 showing a molecular weight of about 76,000-87,000 daltons on SDS-PAGE and an isoelectric point of about 3.6-4.6 on isoelectrophoresis. The results indicate that the present enzyme can be prepared by recombinant DNA technology, and the yield is significantly increased thereby.

Example 2

Preparation of complementary DNA derived from enzyme M-11 and determination of its base sequence and amino acid sequence

Two μg of the recombinant DNA pBMT7 obtained by the method in Example 1-2 was weighed, admixed with 2 M aqueous sodium hydroxide solution to effect degeneration, and admixed with an adequate amount of cold ethanol, followed by collecting the resultant sediment containing a template DNA and drying the sediment in vacuo. To the template DNA were added 50 pmole/ml of a chemically synthesized primer 1 having the base sequence as shown in SEQ ID NO:7, and 10 μl of 40 mM Tris-HCl buffer (pH 7.5) containing 20 mM magnesium chloride and 50 mM sodium chloride, and incubated at 65°C for 2 min to effect annealing, and the mixture was admixed with 2 μl of an aqueous solution containing dATP, dGTP and dTTP in respective amounts of 7.5 μM, 0.5 μl of [α-^{32}P]dCTP (2 mCi/ml), one μl of 0.1 M dithiothreitol, and 2 μl of 1.5 units/ml T7 DNA polymerase, followed by incubating the resultant mixture at 25°C for 5 min to extend the primer 1 from the 5'-terminus to the 3'-terminus. Thus, a complementary chain DNA was formed.

The reaction product containing the complementary chain DNA was divided into quarters, to each of which 2.5 μl of 50 mM aqueous sodium chloride solution containing 80 μM dNTP and 8 μM ddATP, ddCTP, ddGTP or ddTTP was added, and the resultant mixture was incubated at 37°C for 5 min, followed by suspending the reaction by the addition of 4 μl of 95 v/v % aqueous formamide solution containing 20 mM EDTA, 0.05 w/v % bromophenol blue and 0.05 w/v % xylene cyanol. The reaction mixture was placed in a container, heated in a boiling-water bath for 3 min, placed on a gel containing 6 w/v % polyacrylamide, and electrophoresed by energizing the gel with a constant voltage of about 2,000 volts to separate DNA fragments, followed by fixing the gel in usual manner, drying and subjecting the resultant gel to autoradiography.

Analyses of the DNA fragments separated on the radiogram revealed that the complementary chain DNA contains the base sequence consisting of 2,936 base pairs as shown in SEQ ID NO:10. An amino acid sequence estimable from the base sequence was as shown in SEQ ID NO:10, and it was compared with the amino acid sequence containing the N-terminal and the partial amino acid sequence of enzyme M-11 as shown in SEQ ID NO:12, 14 or 15, and found that the amino acid sequence containing the N-terminal of SEQ ID NO:12 corresponded to the amino acid sequence at positions from 1 to 20 of SEQ ID NO:10, and the partial amino acid sequence of SEQ ID NO:14 or 15 corresponded to the amino acid sequence at positions from 486 to 506 or at positions from 606 to 626 of SEQ ID NO:10. The results indicate that the enzyme produced from *Rhizobium* sp. M-11 has the amino acid sequence of SEQ ID NO:2, and the enzyme derived from the microorganism is encoded by the DNA having the base sequence as shown in SEQ ID NO:1.

Example 3

Preparation of recombinant DNA containing DNA derived from *Arthrobacter* sp. Q36 and transformant

Example 3-1

Preparation of chromosomal DNA

Similarly as in Example 1-1, a chromosomal DNA was isolated from *Arthrobacter* sp. Q36, purified and dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the resultant solution was freezed at -80°C.

Example 3-2

Preparation of recombinant DNA pBQT13 and transformant BQT13

The purified chromosomal DNA obtained in Example 3-1 was partially digested similarly as in Example 1-2, followed by recovering a DNA fragment consisting of about 3,000-6,000 base pairs by sucrose density gradient ultracentrifugation. The DNA fragment was ligated to a lysate of Bluescript II SK(+) which had been treated with *Bam* HI similarly as in Example 1-2, and the resultant recombinant DNA was introduced into *Escherichia coli* XLI-Blue. The transformants thus obtained were cultured similarly as in Example 1-2 in an agar plate containing 5-bromo-4-chloro-3-indolyl-β-D-galactoside, and the resultant about 4,500 colonies were fixed on a nylon film, while probe 3 having the base sequence as shown in SEQ ID NO:8 was chemically synthesized based on the amino acid sequence as expressed by Phe-Asp-Val-Asp-Trp-Asp, which are located at positions from 11 to 16 in the amino acid sequence of the peptide fragment D as shown in SEQ ID NO:17, labelled with ^{32}P, and hybridized with transformant colonies which had been fixed on the nylon film, followed by selecting 8 transformants which strongly hybridized with probe 3.

Similarly as in Example 1-2, the objective recombinant DNA was selected from the 8 transformants, and hybridized with probe 4 having the base sequence as shown in SEQ ID NO:9 which had been chemically synthesized based on the amino acid sequence located at positions from 16 to 20, i.e. Thr-Glu-Phe-Trp-Asp, in SEQ ID NO:16, followed by selecting a recombinant DNA which strongly hybridized with probe 4. The recombinant DNA and transformant thus selected were respectively named pBQT13 and BQT13.

The transformant BQT13 was inoculated into L-broth containing ampicillin, and cultured similarly as in Example 3-2, and the proliferated cells were collected from the resultant culture, and from which a recombinant DNA was extracted, purified and analyzed to reveal that the recombinant pBQT13 consists of about 7,200 base pairs and has a structure expressed by the restriction map as shown in FIG. 10. As shown in FIG. 3, it was reveal that the DNA, which consists of 2,325 base pairs and encodes the DNA of enzyme Q36, is located in the downstream near the cleavage site of *Xmn* I.

Example 3-3

Production of enzyme by transformant BQT13

A liquid culture medium consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50 μg/ml ampicillin, autoclaved at 120°C for 20 min, cooled and inoculated with a seed culture of the transformant BQT13 obtained in Example 3-2, followed by culturing the transformant at 37°C for 24 hours by a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 2,450 units of the enzyme.

As a control, *Escherichia coli* XLI-Blue or *Arthrobacter* sp. Q36 was inoculated in a fresh preparation of the same liquid culture medium but free of ampicillin, and cultured and treated similarly as above except that the culturing temperature was set to 30°C. The assay of the activity of the resultants showed that one L of the culture of *Arthrobacter* sp. Q36 yielded about 1,200 units of the enzyme, and the level of which was significantly lower than that of the transformant BQT13. *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BMT7 was purified similarly as in Experiment 1-1, and examined on the properties and characteristics. As a result, it was revealed that it has substantially the same physicochemical properties as shown in Experiment 2 of a molecular weight of about 76,000-87,000 daltons on SDS-PAGE and an isoelectric point of about 3.6-4.6 on isoelectrophoresis.

The results indicate that the enzyme can be prepared by recombinant DNA technology, and the yield might be significantly increased thereby.

Example 4

Preparation of complementary chain DNA derived from *Arthrobacter* sp. Q36, and determination of its base sequence and amino acid sequence

The recombinant DNA pBQT13 obtained in Example 3-2 was similarly treated as in Example 2 to form a template DNA which was then annealed together with the primer 1, followed by allowing T7 DNA polymerase

to act on the resultant to extend the primer 1 from the 5'-terminus to 3'-terminus to obtain a complementary chain DNA. Similarly as in Example 2, the complementary chain DNA was subjected to the dideoxy chain terminator method to analyze DNA fragments isolated on a radiogram. The result revealed that the complementary chain DNA contained a base sequence consisting of 3,073 base pairs and an amino acid sequence estimable from the base sequence were as shown in SEQ ID NO:11. The amino acid sequence was compared with respect to the amino acid sequence containing the N-terminal and the partial amino acid sequence of SEQ ID NO:13, 16 or 17, and found that the amino acid sequence containing the N-terminal of SEQ ID NO:13 corresponded to that located at positions from 1 to 20 in SEQ ID NO:11, and the partial amino acid sequence of SEQ ID NO:16 and 17 corresponded to the amino acid sequence located at positions from 606 to 625 or from 110 to 129 in SEQ ID NO:11. The results indicate that enzyme Q36 has the amino acid sequence of SEQ ID NO:4, and it is encoded by the DNA having the base sequence as shown in SEQ ID NO:3.

Example 5

Preparation of recombinant enzyme

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate, and to each flask was added 50 μg/ml ampicillin and autoclaved at 120°C for 20 min. Thereafter, the flasks were cooled and inoculated with the transformant BMT7 obtained in Example 1-2, followed by culturing the transformant at 27°C for 24 hours by a rotary shaker. Apart from this, 18 L of a fresh preparation of the same liquid culture medium was placed in an Erlenmeyer flask, admixed with 50 μg/ml ampicillin, sterilized at 120°C for 20 min, cooled and inoculated with one v/v % of the seed culture obtained in the above, followed by the culture at 37°C for 24 hours under aeration and agitation conditions. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to show that one L of the culture yielded about 3,000 units of the enzyme. The supernatant was purified by the method in Experiment 1-1 to obtain an about 50 ml aqueous solution containing about 135 units/ml of a recombinant enzyme having a specific activity of about 200 units/mg protein.

Example 6

Preparation of recombinant enzyme

Recombinant BQT13 obtained by the method in Example 3-2 was cultured similarly as in Example 5, and the resultant culture was treated with an ultrasonic integrator to disrupt cells. The resultant suspension was centrifuged to remove insoluble substances, and the resultant supernatant was assayed for the enzyme activity to reveal an enzyme production of about 2,450 units per L of the culture. The supernatant was purified by the method in Experiment 1-1 to obtain an about 45 ml aqueous solution containing about 120 units/ml of a recombinant enzyme having a specific activity of about 200 units/mg protein.

Example 7

Conversion of starch hydrolysate by recombinant enzyme

A potato starch was suspended in water to give a 6 w/w % suspension which was then autoclaved at 120°C for 10 min to gelatinize the starch. The gelatinized starch was rapidly cooled to 50°C, adjusted to a pH of about 4.5, admixed with 2,500 units/g starch, d.s.b., of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted at 50°C for 20 hours. The reaction mixture was adjusted to pH 6.0, autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, admixed with 150 units/g starch, d.s.b., of "TERMAMYL 60L", an α-amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 45°C for 24 hours to obtain a reaction mixture containing reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The reaction mixture was autoclaved at 120°C for 20 min to inactivate the remaining enzyme, rapidly cooled to 45°C, admixed with one unit/g starch, d.s.b., of the recombinant enzyme obtained in Example 5, and enzymatically reacted at 45°C for 96 hours. The resultant reaction mixture was heated at 96°C for 10 min to inactivate the remaining enzyme, cooled and filtered, and the resultant filtrate was in usual manner decolored with an activated charcoal, de-

salted and purified by an ion exchanger and concentrated to obtain an about 70 w/w % syrup, d.s.b., in a yield of about 91%, d.s.b.

Analysis of the syrup conducted by the method of Experiment 2-1 revealed that it had a DE (dextrose equivalent) of 18.7 and contained as a main component, on a dry solid basis, 8.4 w/w % α-glucosyl trehalose, 5.6 w/w % α-maltosyl trehalose, 37.9 w/w % α-maltotriosyl trehalose, and that the greater part of the aforesaid reducing saccharides were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 8

Conversion of starch hydrolysate by recombinant enzyme

Potato starch was suspended in water to give a concentration of 33 w/w %, d.s.b., and the suspension was admixed with 0.1 w/w % calcium carbonate, d.s.b. The resultant suspension was admixed with 0.2 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an α-amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95°C for 15 min. The reaction mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled, admixed with 5 units/g starch, d.s.b., of a maltotetraose-forming amylase derived from *Pseudomonas stutzeri* as disclosed in Japanese Patent Laid-Open No.240,784/88, and enzymatically reacted at 55°C for 6 hours. Thereafter, the resultant reaction mixture was admixed with 30 units/g starch, d.s.b., of "α-amylase 2A", an α-amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, and enzymatically reacted at 65°C for 4 hours to form about 50 w/w %, d.s.b., of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The resultant mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of the recombinant enzyme obtained in Example 5, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain a syrupy product with a concentration of about 70 w/w %, d.s.b., in a yield of about 90% against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 10.5 and contained as a main component 3.8 w/w % α-glucosyl trehalose, 43.8 w/w % a-maltosyl trehalose, and 1.2 w/w % α-maltotriosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained therein were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 9

Conversion of maltopentaose by recombinant enzyme

A high-purity maltopentaose produced by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, was dissolved in water to give a concentration of 20 w/w %, d.s.b., and the solution was adjusted to pH 6.5, admixed with one unit/g maltopentaose, d.s.b., of a recombinant enzyme obtained by the method in Example 5, and enzymatically reacted at 45°C for 48 hours. The reaction mixture was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, concentrated and analyzed by the method in Experiment 2-1 to find that about 92 w/w %, d.s.b., of the material maltopentaose was converted into α-maltotriosyl trehalose.

Four jacketed-stainless steel columns, having a diameter of 5.4 cm and a length of 5 m each, were packed to homogeneity with "XT-1016 (Na^+-form)", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series to give a total column length of 20 m. The reaction mixture obtained in the above was fed to the columns at a rate of about 5 v/v % against the resin at an inner column temperature of 55°C, and the columns were fed with 55°C hot water at an SV (space velocity) of 0.13 to elute saccharide components. Based on the saccharide composition analysis of the eluate,

fractions rich in non-reducing saccharides were collected, pooled, concentrated, dried *in vacuo* and pulverized to obtain a solid product in a yield of about 55%, d.s.b.

Analysis of the solid product by the method in Experiment 2-1 revealed that it had a DE less than about 0.2 and contained 99.0 w/w % α-maltotriosyl trehalose, d.s.b. The product, having a relatively-low hygroscopicity, a significantly-low reducibility as well as a slight sweetness, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 10

Conversion of starch hydrolysate by recombinant enzyme

"PINE-DEX #4", a starch hydrolysate produced by Matsutani Chemical Ind., Co., Ltd., Kyoto, Japan, was dissolved in water to give a concentration of 40 w/w %, d.s.b., and the solution was heated to 45°C, adjusted to pH 6.5, admixed with one unit/g starch hydrolysate, d.s.b., of a recombinant enzyme obtained by the method in Example 5, and enzymatically reacted at for 96 hours to obtain a reaction mixture containing non-reducing saccharides having trehalose structure as an end unit. Thereafter, the reaction mixture was heated at 100°C for 10 min to inactivate the remaining enzyme, concentrated up to a 20 w/w % solution, d.s.b., cooled to 55°C, adjusted to pH 4.5, admixed with 10 units/g saccharide, d.s.b., of "GLUCOZYME", a glucoamylase specimen commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, and enzymatically reacted for 40 hours. The reaction mixture was heated at 100°C for 10 min to inactivate the remaining enzyme, cooled, decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain an about 60 w/w % syrupy product containing about 29.7 w/w % trehalose, d.s.b.

Similarly as in Example 9 except for using "CG6000 (Na^+-form), the syrupy product was fractionated, followed by collecting fractions containing about 90 w/w % trehalose, d.s.b. The fractions were pooled, concentrated into an about 75 w/w % solution which was then transferred to a crystallizer, admixed with about 2 w/w % trehalose hydrate as a seed crystal against saccharides, d.s.b., and crystallized under gentle stirring conditions to obtain a massecuite with a crystallinity of about 45%. The massecuite was sprayed downward from a nozzle, equipped at the upper part of a spraying tower at a pressure of about 150 kg/cm^2 while about 85°C hot air was flowing downward from the upper part of the tower to accumulate a crystalline powder on a belt conveyer provided on the basement of the tower, followed by gradually transferring it out of the tower. Thereafter, the powder was transferred to an aging tower and aged for 10 hours to complete the crystallization and drying while an about 40°C hot air was blowing to the contents.

The product, having a substantial non-hygroscopicity and a mild and high-quality sweetness, can be satisfactorily used in food products, cosmetics, pharmaceuticals and feeds as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

Example 11

Conversion of starch hydrolysate by recombinant enzyme

Tapioca starch was suspended in water to give a concentration of 34 w/w % and admixed with 0.1 w/w % calcium carbonate. To the suspension was added 0.2 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an α-amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95°C for 15 min to liquefy the starch. The liquefied product was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 55°C, adjusted to pH 5.2, admixed with 10 units/g starch, d.s.b., of "α-amylase 2A", an α-amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, and 500 units of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted at 55°C for 20 hours to form a mixture with a DE of about 29, containing about 60 w/w %, d.s.b., of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose and maltohexaose. The mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of a recombinant enzyme obtained by the method in Example 6, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain a syrupy product with a concentration of about 70 w/w %, d.s.b., in a yield of about 90% against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 15.8 and contained as a main component 5.8 w/w % α-glucosyl trehalose, 8.5 w/w % a-maltosyl trehalose, 13.1 w/w % α-maltotriosyl trehalose, 18.9 w/w % α-maltotetraosyl trehalose and 3.6 w/w % α-maltopentaosyl trehalose. d.s.b., and that most of the reducing amylaceous saccharides contained therein were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 12

Conversion of starch hydrolysate by recombinant enzyme

Similarly as in Example 8, a liquefied potato starch was successively subjected to the action of maltotetraose-forming amylase and α-amylase to form a mixture containing about 50 w/w %, d.s.b, of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The reaction mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of a recombinant enzyme obtained by the method in Example 6, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled and filtered, and the filtrate was decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain an about 70 w/w % syrupy product in a yield of about 90 w/w % against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 10.3 and contained as a main component 3.6 w/w % α-glucosyl trehalose, 44.0 w/w % α-maltosyl trehalose and 1.0 w/w % α-maltotriosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained in the syrupy product were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

As is described above, the present invention is based on the finding of a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher. The present invention is to explore a way to produce such enzyme by recombinant DNA technology in a relatively-large scale and in a considerably-high yield. The conversion method using the present recombinant enzyme effectively converts reducing amylaceous saccharides into their corresponding non-reducing saccharides which have a mild and high-quality sweetness and an adequate viscosity and moisture-retaining ability, do not have a reducing residue within the molecules, and sweeten food products without fear of causing an unsatisfactory coloration and deterioration. In addition, the present recombinant enzyme is the one with a revealed total amino acid sequence, and because of this it can be used for the preparation of trehalose and non-reducing saccharides having trehalose structure as an end unit which are premised on being used in food products without fear of causing side effects.

Thus, the present invention is a significant invention which exerts the aforesaid outstanding action and effect as well as giving a great contribution to the field.

While there has been described what is at present considered to be the preferred embodiments of the invention, it will be understood the various modifications may be made therein, and it is intended to cover in the appended claims all such modifications as fall within the true spirits and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO

(ii) TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES

(iii) NUMBER OF SEQUENCES: 17

(iv) ADDRESS:
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(C) CITY: OKAYAMA
(E) COUNTRY: JAPAN
(F) POSTAL CODE (ZIP): 700

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(vii) PRIOR APPLICATION DATA:
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(B1) FILING DATE: February 23, 1994
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(B3) FILING DATE: April 6, 1994
(A4) APPLICATION NUMBER: JP 90728/1994
(B4) FILING DATE: April 6, 1994

(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2316 base pairs
(B) TYPE: nucleic acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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(3) INFORMATION FOR SEQ ID NO:2:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:772
          (B) TYPE:amino acid
          (D) TOPOLOGY:linear
     (ii) MOLECULE TYPE:peptide
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:2:
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(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2325 base pairs
(B) TYPE: nucleic acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620
CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740
GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920
GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040
CTGTTCACGG GGTACCGGCC GGTCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220
GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA                2325
```

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 775
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1               5                   10                  15
Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
        20                  25                  30
Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
35                  40                  45                  50
Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
                55                  60                  65
Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
    70                  75                  80                  85
```

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
90 95 100
Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
105 110 115
Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
120 125 130 135
Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
140 145 150
Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
155 160 165 170
Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185
Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200
Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
205 210 215 220
Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235
Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285
Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
290 295 300 305
Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
310 315 320
Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340
Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
345 350 355
Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
360 365 370
Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
375 380 385 390
Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
395 400 405
Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425
Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440
Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
445 450 455
Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490
Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
495 500 505 510
Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
515 520 525
Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
545 550 555 560
Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
565 570 575
Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
580 585 590 595
Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610
Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
615 620 625

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Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
630                 635                 640                 645
Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
            650                 655                 660
Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
    665                 670                 675                 680
Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
                685                 690                 695
Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
        700                 705                 710
Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
715                 720                 725                 730
Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
            735                 740                 745
Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
    750                 755                 760                 765
Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
                770                 775
```

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:14 base pairs
(B) TYPE:nucleic acid
(C) STRANDEDNESS:single
(D) TOPOLOGY:unknown

(ii) MOLECULE TYPE:other nucleic acid
(A) probe

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCNGARTGGG ARAA 14

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:14 base pairs
(B) TYPE:nucleic acid
(C) STRANDEDNESS:single
(D) TOPOLOGY:unknown

(ii) MOLECULE TYPE:other nucleic acid
(A) probe

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACNGARTTYT GGGA 14

(8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:17 base pairs
(B) TYPE:nucleic acid
(C) STRANDEDNESS:single
(D) TOPOLOGY:unknown

(ii) MOLECULE TYPE:other nucleic acid
(A) primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTAAAACGAC GGCCAGT 17

(9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:17 base pairs
(B) TYPE:nucleic acid
(C) STRANDEDNESS:single
(D) TOPOLOGY:unknown

(ii) MOLECULE TYPE:other nucleic acid
(A) probe

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTYGAYGTNG AYTGGGA 17

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:14 base pairs
(B) TYPE:nucleic acid
(C) STRANDEDNESS:single
(D) TOPOLOGY:unknown

(ii) MOLECULE TYPE:other nucleic acid
(A) probe

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

ACNGARTTYT GGGA 14

(11) INFORMATION FOR SEQ ID NO:10:
(i)SEQUENCE CHARACTERISTICS:
(A)LENGTH:2936 base pairs
(B)TYPE:nucleic acid
(C)strandedness:double
(D)TOPOLOGY:linear
(ii)MOLECULE TYPE:genomic DNA
(vi)ORIGINAL SOURCE:
(A)ORGANISM:Rhizobium sp.
(B)INDIVIDUAL ISOLATE:M-11 (FERM BP-4130)
(ix)FEATURE:
(A)NAME/KEY:5'UTR
(B)LOCATION:1..564
(C)IDENTIFICATION METHOD:E
(A)NAME/KEY:mat peptide
(B)LOCATION:565..2880
(C)IDENTIFICATION METHOD:S
(A)NAME/KEY:3'UTR
(B)LOCATION:2881..2936
(C)IDENTIFICATION METHOD:E
(xi)SEQUENCE DESCRIPTION:SEQ ID NO:10:

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60
CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120
CCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180
CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240
TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300

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GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA  360
GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC  420
GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA  480
CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC  540
AGGCAAGCAG GGCGGGACGG GCTC                                         564
ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC  612
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
1               5                   10                  15
ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG  660
Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
            20                  25                  30
GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC  708
Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
        35                  40                  45
GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC  756
Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
    50                  55                  60
GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC  804
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
65                  70                  75                  80
GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG  852
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
                85                  90                  95
TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC  900
Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
            100                 105                 110
GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG  948
Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
        115                 120                 125
GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG  996
Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
    130                 135                 140
CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG  1044
Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145                 150                 155                 160
CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC  1092
Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
                165                 170                 175
GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA  1140
Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
            180                 185                 190
CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG  1188
Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg
        195                 200                 205
GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC  1236
Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
    210                 215                 220
TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC  1284
Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
225                 230                 235                 240
GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC  1332
Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
                245                 250                 255
GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG  1380
Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
            260                 265                 270
TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC  1428
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
        275                 280                 285
GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG  1476
Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
    290                 295                 300
GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG  1524
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Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
305                 310                 315                 320
GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC     1572
Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                325                 330                 335
TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT     1620
Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
            340                 345                 350
CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC     1668
Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
        355                 360                 365
CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG     1716
Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
    370                 375                 380
GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC     1764
Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
385                 390                 395                 400
CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC     1812
Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
                405                 410                 415
AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC     1860
Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
            420                 425                 430
ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC     1908
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
        435                 440                 445
GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG     1956
Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
    450                 455                 460
ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC     2004
Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465                 470                 475                 480
ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG     2052
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
                485                 490                 495
ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC     2100
Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
            500                 505                 510
ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG     2148
Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
        515                 520                 525
GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC     2196
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
    530                 535                 540
GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT     2244
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
545                 550                 555                 560
CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC     2292
Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
                565                 570                 575
TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC     2340
Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
            580                 585                 590
CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG     2388
Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
        595                 600                 605
CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG     2436
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
    610                 615                 620
GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC     2484
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
625                 630                 635                 640
GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC     2532
Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
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645 650 655
TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580
Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
660 665 670
CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628
Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
675 680 685
CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676
His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
690 695 700
GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724
Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
705 710 715 720
CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772
Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
725 730 735
ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820
Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
740 745 750
TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868
Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
755 760 765
GGA GGC AAG TCA 2880
Gly Gly Lys Ser
770
TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936

(12) INFORMATION FOR SEQ ID NO:11:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:3084 base pairs
(B) TYPE:nucleic acid
(C) strandedness:double
(D) TOPOLOGY:linear
(ii) MOLECULE TYPE:genomic DNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM:Arthrobacter sp.
(B) INDIVIDUAL ISOLATE:Q36 (FERM BP-4316)
(ix) FEATURE:
(A) NAME/KEY:5'UTR
(B) LOCATION:1..677
(C) IDENTIFICATION METHOD:E
(A) NAME/KEY:mat peptide
(B) LOCATION:678..3002
(C) IDENTIFICATION METHOD:S
(A) NAME/KEY:3'UTR
(B) LOCATION:3003..3073
(C) IDENTIFICATION METHOD:E
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:11:

GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60
GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240
TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT 300
CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420
GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480
GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
CCCGCTGGGG AGGACGCC 677
ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe

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1               5                       10                      15
ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC    773
Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
            20                  25                  30
GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC    821
Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
        35                  40                  45
GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC    869
Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
    50                  55                  60
GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG    917
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
65                  70                  75                  80
GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG    965
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
                85                  90                  95
ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC   1013
Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
            100                 105                 110
CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG   1061
Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
        115                 120                 125
GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG   1109
Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
    130                 135                 140
CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG   1157
Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145                 150                 155                 160
CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC   1205
Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
                165                 170                 175
GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG   1253
Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
            180                 185                 190
CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC   1301
Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg
        195                 200                 205
GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC   1349
Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
    210                 215                 220
TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC   1397
Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
225                 230                 235                 240
GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC   1445
Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
                245                 250                 255
GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG   1493
Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
            260                 265                 270
CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC   1541
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
        275                 280                 285
GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG   1589
Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu
    290                 295                 300
GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG   1637
Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln
305                 310                 315                 320
GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC   1685
Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                325                 330                 335
TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT   1733
Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
            340                 345                 350
```

```
TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC    1781
Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
        355                 360                 365
CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG    1829
Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
    370                 375                 380
GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC    1877
Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
385                 390                 395                 400
CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG    1925
Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
            405                 410                 415
CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC    1973
Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
        420                 425                 430
ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC    2021
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
        435                 440                 445
GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG    2069
Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
    450                 455                 460
CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC    2117
Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465                 470                 475                 480
ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC    2165
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
            485                 490                 495
ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC    2213
Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
        500                 505                 510
GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG    2261
Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
        515                 520                 525
GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC    2309
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
    530                 535                 540
GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT    2357
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
545                 550                 555                 560
CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG    2405
Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
            565                 570                 575
TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC    2453
Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
        580                 585                 590
CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG    2501
Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
        595                 600                 605
CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG    2549
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
    610                 615                 620
GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC    2597
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
625                 630                 635                 640
GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG    2645
Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
            645                 650                 655
TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG    2693
Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
        660                 665                 670
CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC    2741
Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
        675                 680                 685
CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC    2789
```

```
Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
    690                 695                     700
ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC    2837
Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
705                 710                     715                 720
GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC    2885
Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
                725                 730                     735
ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA    2933
Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
            740                 745                     750
GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG    2981
Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
        755                 760                     765
CCG CAG ACA GGA GGA GAG TCA                                        3002
Pro Gln Thr Gly Gly Glu Ser
    770                 775
TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
TCTGGGCGCC C                                                      3073
```

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1               5                   10                  15
Leu Phe Asp
        20
```

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1               5                   10                  15
Leu Phe Asp
        20
```

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS :

(A) LENGTH: 21

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val Ile Ala Glu Val Ala Pro
1               5                   10                  15
Glu Trp Glu Lys
        20
```

```
(16)INFORMATION FOR SEQ ID NO:15:
     (i)SEQUENCE CHARACTERISTICS:
          (A)LENGTH:21
          (B)TYPE:amino acid
          (D)TOPOLOGY:linear
     (ii)MOLECULE TYPE:peptide
     (v)FRAGMENT TYPE:internal fragment
     (xi)SEQUENCE DESCRIPTION:SEQ ID NO:15:

Leu Val Gln Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu
1               5                   10                  15
Phe Trp Asp Arg
        20

(17)INFORMATION FOR SEQ ID NO:16:
     (i)SEQUENCE CHARACTERISTICS:
          (A)LENGTH:20
          (B)TYPE:amino acid
          (D)TOPOLOGY:linear
     (ii)MOLECULE TYPE:peptide
     (v)FRAGMENT TYPE:internal fragment
     (xi)SEQUENCE DESCRIPTION:SEQ ID NO:16:

Leu Val Gln Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu
1               5                   10                  15
Phe Trp Asp
        20

(18)INFORMATION FOR SEQ ID NO:17:
     (i)SEQUENCE CHARACTERISTICS:
          (A)LENGTH:20
          (B)TYPE:amino acid
          (D)TOPOLOGY:linear
     (ii)MOLECULE TYPE:peptide
     (v)FRAGMENT TYPE:internal fragment
     (xi)SEQUENCE DESCRIPTION:SEQ ID NO:17:

Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu
1               5                   10                  15
Ala Gly Gly
        20
```

Claims

1. A DNA encoding an enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.

2. The DNA as claimed in claim 1, wherein said enzyme has the following physicochemical properties:
   (1) Molecular weight
   About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
   (2) Isoelectric point (pI)
   About 3.6-4.6 on isoelectrophoresis.

3. The DNA as claimed in claim 1, wherein said enzyme has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and

homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1 5 10 15
Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
20 25 30
Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35 40 45 50
Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65
Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu

```
70                  75                  80                  85
Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
                90                  95                  100
Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
        105                 110                 115
Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
120                 125                 130                 135
Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
            140                 145                 150
Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
    155                 160                 165                 170
Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
                175                 180                 185
Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
        190                 195                 200
Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
205                 210                 215                 220
Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
            225                 230                 235
Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
    240                 245                 250                 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
                260                 265                 270
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
        275                 280                 285
Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
290                 295                 300                 305
Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
            310                 315                 320
```

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340
Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
345 350 355
Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
360 365 370
Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
375 380 385 390
Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
395 400 405
Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425
Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440
Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
445 450 455
Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490
Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
495 500 505 510
Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
515 520 525
Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
530 535 540
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
545 550 555 560
Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp

565 570 575

Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro

580 585 590 595

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu

630 635 640 645

Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His

685 690 695

Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg

700 705 710

Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu

715 720 725 730

Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly

735 740 745

Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val

750 755 760 765

Pro Ala Thr Gly Gly Lys Ser

770

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
20 25 30
Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
35 40 45 50
Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65
Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
70 75 80 85
Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
90 95 100
Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
105 110 115
Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
120 125 130 135
Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
140 145 150
Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
155 160 165 170
Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185
Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200
Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
205 210 215 220
Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235
Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala

275 280 285

Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg

290 295 300 305

Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile

310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu

325 330 335 340

Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly

345 350 355

Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp

445 450 455

Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg

495 500 505 510

Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
545 550 555 560

Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
565 570 575

Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
580 585 590 595

Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
700 705 710

Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
715 720 725 730

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
735 740 745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

770 775

4. The DNA as claimed in claim 1, which has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

SEQ ID NO:1

```
ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT   60
GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC  120
ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG  180
GACCCGGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC  240
GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGCAG  300
AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC  360
GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC  420
GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG  480
CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC  540
TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG  600
GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG  660
GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC  720
GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC  780
CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA  840
GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA  900
CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG  960
GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140
ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200
```

CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
TTTCACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620
CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
CCGGACCCGG CATTCGAGGA GGCACTTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
GAGGTGCGTG CGGAACTTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TGCGTCCAAC 1800
TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860
ACCGAGTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GGCGCCCCTT CAGCTTCGCC 1920
GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TGCGGCGGAA CCGGCCCGAG 2040
CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100
TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
CAGTCGGGCG GCTGGCGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCCG 2280
GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

SEQ ID NO:3

```
ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC  60
GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
```

CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540
TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600
GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660
GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC 720
GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780
CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900
CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200
CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620
CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740
GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920
GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040
CTGTTCACGG GGTACCGGCC GGTCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220

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GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280

TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA                 2325
```

5. The DNA as claimed in claim 4, wherein one or more bases in SEQ ID NO:1 or 3 are replaced with other bases by means of degeneracy of genetic code without alternating the amino acid sequence of the following SEQ ID NO:2 or 4:

```
SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1               5                   10                  15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
        20                  25                  30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35                  40                  45                  50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
            55                  60                  65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
    70                  75                  80                  85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
                90                  95                  100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
        105                 110                 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
120                 125                 130                 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
            140                 145                 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
    155                 160                 165                 170

Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
                175                 180                 185
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Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200
Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
205 210 215 220
Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235
Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285
Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
290 295 300 305
Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
310 315 320
Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340
Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
345 350 355
Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
360 365 370
Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
375 380 385 390
Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
395 400 405
Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425
Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu

445 450 455

Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg

495 500 505 510

Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro

545 550 555 560

Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp

565 570 575

Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro

580 585 590 595

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu

630 635 640 645

Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
685 690 695

Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
700 705 710

Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
715 720 725 730

Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
735 740 745

Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
750 755 760 765

Pro Ala Thr Gly Gly Lys Ser
770

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu

120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg

140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp

155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg

175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu

205 210 215 220

Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His

225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val

240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala

275 280 285

Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg

290 295 300 305

Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile

310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu

325 330 335 340

Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly

345 350 355

Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
375 380 385 390
Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
395 400 405
Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425
Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440
Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
445 450 455
Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490
Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
495 500 505 510
Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
515 520 525
Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
545 550 555 560
Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
565 570 575
Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
580 585 590 595
Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610
Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu

630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His

685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

700 705 710

Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr

715 720 725 730

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe

735 740 745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

770 775

6. The DNA as claimed in claim 1, which has the base sequence as shown in the following SEQ ID NO:10 or 11:

SEQ ID NO:10:

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60

CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120

GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180

CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240

TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300

GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360

GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420

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GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA  480
CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC  540
AGGCAAGCAG GGCGGGACGG GCTC                                         564
ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC   612
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
1               5                   10                  15
ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG   660
Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
            20                  25                  30
GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC   708
Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
        35                  40                  45
GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC   756
Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
    50                  55                  60
GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC   804
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
65                  70                  75                  80
GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG   852
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
                85                  90                  95
TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC   900
Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
            100                 105                 110
GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG   948
Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
        115                 120                 125
GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG   996
Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
```

130 135 140

CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044

Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro

145 150 155 160

CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092

Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His

165 170 175

GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140

Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu

180 185 190

CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188

Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg

195 200 205

GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236

Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg

210 215 220

TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284

Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp

225 230 235 240

GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332

Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr

245 250 255

GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG 1380

Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu

275 280 285

GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476

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Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
    290                 295                 300

GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG   1524
Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
305                 310                 315                 320

GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC   1572
Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                325                 330                 335

TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT   1620
Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
            340                 345                 350

CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC   1668
Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
        355                 360                 365

CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG   1716
Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
    370                 375                 380

GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC   1764
Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
385                 390                 395                 400

CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC   1812
Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
                405                 410                 415

AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC   1860
Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
            420                 425                 430

ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC   1908
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
        435                 440                 445
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GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
450 455 460

ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465 470 475 480

ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
485 490 495

ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
500 505 510

ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
515 520 525

GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
530 535 540

GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
545 550 555 560

CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
565 570 575

TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
580 585 590

CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln

595 600 605

CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436

Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp

610 615 620

GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484

Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala

625 630 635 640

GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532

Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp

645 650 655

TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580

Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu

660 665 670

CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628

Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val

675 680 685

CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676

His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly

690 695 700

GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724

Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu

705 710 715 720

CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772

Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met

725 730 735

ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820

Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu

740 745 750

TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868

Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
755 760 765

GGA GGC AAG TCA 2880
Gly Gly Lys Ser
770

TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936

SEQ ID NO:11

GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60
GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240
TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT 300
CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420
GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480
GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
CCCGCTGGGG AGGACGC 677

ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
1 5 10 15

ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773
Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
20 25 30

GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821
Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
35 40 45

GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
50 55 60

GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
65 70 75 80

GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
85 90 95

ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
100 105 110

CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
115 120 125

GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
130 135 140

CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145 150 155 160

CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
165 170 175

GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
180 185 190

CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg

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        195                 200                 205
GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC   1349
Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
    210                 215                 220
TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC   1397
Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
225                 230                 235                 240
GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC   1445
Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
                245                 250                 255
GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG   1493
Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
            260                 265                 270
CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC   1541
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
        275                 280                 285
GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG   1589
Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu
    290                 295                 300
GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG   1637
Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln
305                 310                 315                 320
GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC   1685
Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                325                 330                 335
TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT   1733
Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
            340                 345                 350
TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC   1781
```

Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
355 360 365

CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
370 375 380

GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
385 390 395 400

CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
405 410 415

CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
420 425 430

ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
435 440 445

GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
450 455 460

CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465 470 475 480

ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
485 490 495

ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
500 505 510

GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
515 520 525

GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540

GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
545 550 555 560

CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
565 570 575

TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
580 585 590

CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG 2501
Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
595 600 605

CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
610 615 620

GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
625 630 635 640

GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
645 650 655

TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu

```
             660                       665                       670
CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC   2741
Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
         675                       680                       685
CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC   2789
Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
     690                       695                       700
ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC   2837
Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
705                     710                       715                     720
GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC   2885
Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
                 725                       730                       735
ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA   2933
Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
             740                       745                       750
GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG   2981
Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
         755                       760                       765
CCG CAG ACA GGA GGA GAG TCA                                       3002
Pro Gln Thr Gly Gly Glu Ser
     770                       775
TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
TCTGGGCGCC C                                                      3073
```

7. The DNA as claimed in claim 1, which is derived from a microorganism selected from the group consisting of those of the genera *Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium* and *Terrabacter*.

8. A replicable recombinant DNA containing the DNA of claim 1 and a self-replicable vector.

9. The replicable recombinant DNA as claimed in claim 8, wherein said DNA encodes an enzyme having the following physicochemical properties:
   (1) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
(2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.

10. The replicable recombinant DNA as claimed in claim 8, wherein said DNA encodes an enzyme having an amino acid sequence selected from the group consisting of those as shown in SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous base sequences to these amino acid sequences:

```
SEQ ID NO:2
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1               5                   10                  15
Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
        20                  25                  30
Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35                  40                  45                  50
Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
            55                  60                  65
Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
    70                  75                  80                  85
Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
                90                  95                  100
```

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
105 110 115
Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
120 125 130 135
Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
140 145 150
Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
155 160 165 170
Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185
Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200
Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
205 210 215 220
Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235
Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285
Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
290 295 300 305
Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
310 315 320
Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340
Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala

345 350 355

Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu

445 450 455

Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg

495 500 505 510

Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro

545 550 555 560

Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp

565 570 575

Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro

580 585 590 595

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610
Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
615 620 625
Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
630 635 640 645
Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
650 655 660
Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
665 670 675 680
Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
685 690 695
Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
700 705 710
Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
715 720 725 730
Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
735 740 745
Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
750 755 760 765
Pro Ala Thr Gly Gly Lys Ser
770

SEQ ID NO:4

```
Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1               5                   10                  15
Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
        20                  25                  30
Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
```

35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu

70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro

90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala

105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu

120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg

140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp

155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg

175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu

205 210 215 220

Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His

225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val

240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala

275 280 285

Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
290 295 300 305

Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340

Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
345 350 355

Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
360 365 370

Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
375 380 385 390

Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
395 400 405

Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
445 450 455

Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490

Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
495 500 505 510

Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro

545 550 555 560

Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp

565 570 575

Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro

580 585 590 595

Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu

630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His

685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

700 705 710

Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr

715 720 725 730

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe

735 740 745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

770 775

11. The replicable recombinant DNA as claimed in claim 8, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

SEQ ID NO:1

```
ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT   60
GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC  120
ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG  180
GACCCGGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC  240
GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGCAG  300
AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC  360
GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC  420
GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG  480
CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC  540
TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG  600
GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG  660
GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC  720
GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC  780
CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA  840
GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA  900
CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG  960
GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140
ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200
CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
```

CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
TTTCACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620
CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
CCGGACCCGG CATTCGAGGA GGCACTTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
GAGGTGCGTG CGGAACTTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TGCGTCCAAC 1800
TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860
ACCGAGTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GGCGCCCCTT CAGCTTCGCC 1920
GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TGCGGCGGAA CCGGCCCGAG 2040
CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100
TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
CAGTCGGGCG GCTGGCGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCCG 2280
GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

SEQ ID NO:3

ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC 60
GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540
TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600

```
GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG  660
GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC  720
GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC  780
CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA  840
GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC  900
CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG  960
GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200
CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620
CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740
GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920
GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040
CTGTTCACGG GGTACCGGCC GGTCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220
GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA                2325
```

12. The replicable recombinant DNA as claimed in claim 11, wherein one or more bases in SEQ ID NOs:1 and 3 are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences of the following SEQ ID NOs:2 and 4 in this order:

SEQ ID NO:2

```
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1               5                   10                  15
Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
        20                  25                  30
Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35                  40                  45                  50
Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
            55                  60                  65
Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
    70                  75                  80                  85
Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
                90                  95                  100
Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
        105                 110                 115
Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
120                 125                 130                 135
Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
            140                 145                 150
Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
    155                 160                 165                 170
Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
                175                 180                 185
Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
```

190 195 200

Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu

205 210 215 220

Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His

225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val

240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala

275 280 285

Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg

290 295 300 305

Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile

310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu

325 330 335 340

Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala

345 350 355

Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
445 450 455
Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490
Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
495 500 505 510
Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
515 520 525
Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
530 535 540
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
545 550 555 560
Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
565 570 575
Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
580 585 590 595
His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610
Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
615 620 625
Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
630 635 640 645
Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
650 655 660
Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
665 670 675 680
Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His

685 690 695

Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg

700 705 710

Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu

.715 720 725 730

Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly

735 740 745

Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val

750 755 760 765

Pro Ala Thr Gly Gly Lys Ser

770

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp

20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly

35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu

70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro

90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala

105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu

120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
205 210 215 220

Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285

Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
290 295 300 305

Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340

Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
345 350 355

Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
360 365 370

Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp

445 450 455

Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg

495 500 505 510

Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro

545 550 555 560

Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp

565 570 575

Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro

580 585 590 595

Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
700 705 710

Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
715 720 725 730

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
735 740 745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
770 775

13. The replicable recombinant DNA as claimed in claim 8, which has a base sequence selected from the group consisting of those as shown in SEQ ID NO:10 and 11:

SEQ ID NO:10:

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60

CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120

GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180

CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240

TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300

GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360

GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420

GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA 480

CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540

AGGCAAGCAG GGCGGGACGG GCTC 564

ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
1 5 10 15

ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
20 25 30

GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
35 40 45

GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
50 55 60

GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
65 70 75 80

GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
85 90 95

TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
100 105 110

GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
115 120 125

GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln

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    130                 135                 140
CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG   1044
Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145                 150                 155                 160
CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC   1092
Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
                165                 170                 175
GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA   1140
Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
            180                 185                 190
CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG   1188
Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg
        195                 200                 205
GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC   1236
Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
    210                 215                 220
TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC   1284
Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
225                 230                 235                 240
GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC   1332
Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
                245                 250                 255
GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG   1380
Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
            260                 265                 270
TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC   1428
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
        275                 280                 285
GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG   1476
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Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
    290                     295                     300
GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG   1524
Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
305                     310                     315                     320
GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC   1572
Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                325                     330                     335
TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT   1620
Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
            340                     345                     350
CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC   1668
Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
        355                     360                     365
CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG   1716
Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
    370                     375                     380
GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC   1764
Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
385                     390                     395                     400
CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC   1812
Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
                405                     410                     415
AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC   1860
Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
            420                     425                     430
ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC   1908
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
        435                     440                     445
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GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
450 455 460

ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465 470 475 480

ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
485 490 495

ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
500 505 510

ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
515 520 525

GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
530 535 540

GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
545 550 555 560

CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
565 570 575

TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
580 585 590

CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln

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        595                 600                 605
CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG   2436
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
    610                 615                 620
GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC   2484
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
625                 630                 635                 640
GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC   2532
Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
                645                 650                 655
TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG   2580
Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
            660                 665                 670
CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG   2628
Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
        675                 680                 685
CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC   2676
His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
    690                 695                 700
GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA   2724
Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
705                 710                 715                 720
CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG   2772
Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
                725                 730                 735
ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG.  2820
Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
            740                 745                 750
TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA   2868
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Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
        755                     760                     765

GGA GGC AAG TCA                                                     2880
Gly Gly Lys Ser
    770

TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC       2936
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SEQ ID NO:11

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GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG  60
GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240
TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT 300
CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420
GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480
GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
CCCGCTGGGG AGGACGC                                                677

ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC   725
Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
1               5                   10                  15

ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC   773
Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
            20                  25                  30

GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC   821
Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
        35                  40                  45
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GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
50 55 60

GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
65 70 75 80

GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
85 90 95

ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
100 105 110

CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
115 120 125

GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
130 135 140

CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145 150 155 160

CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
165 170 175

GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
180 185 190

CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg

195 200 205

GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349

Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg

210 215 220

TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397

Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp

225 230 235 240

GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445

Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr

245 250 255

GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493

Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC 1541

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu

275 280 285

GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589

Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu

290 295 300

GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637

Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln

305 310 315 320

GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685

Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His

325 330 335

TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733

Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val

340 345 350

TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781

Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
355 360 365

CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
370 375 380

GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
385 390 395 400

CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
405 410 415

CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
420 425 430

ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
435 440 445

GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
450 455 460

CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465 470 475 480

ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
485 490 495

ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
500 505 510

GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
515 520 525

GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540

GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
545 550 555 560

CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
565 570 575

TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
580 585 590

CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG 2501
Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
595 600 605

CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
610 615 620

GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
625 630 635 640

GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
645 650 655

TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu

```
            660                 665                 670
CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC   2741
Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
        675                 680                 685
CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC   2789
Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
    690                 695                 700
ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC   2837
Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
705                 710                 715                 720
GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC   2885
Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
                725                 730                 735
ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA   2933
Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
            740                 745                 750
GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG   2981
Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
        755                 760                 765
CCG CAG ACA GGA GGA GAG TCA                                       3002
Pro Gln Thr Gly Gly Glu Ser
    770                 775
TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
TCTGGGCGCC C                                                      3073
```

14. The replicable recombinant DNA as claimed in claim 8, wherein said DNA is derived from a microorganism selected from the group consisting of those of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*.

15. The recombinant DNA as claimed in claim 8, wherein said self-replicable vector is a plasmid vector Bluescript II SK(+).

16. A transformant obtainable by introducing into a suitable host a recombinant DNA containing the DNA of claim 1 and a self-replicable vector.

17. The transformant as claimed in claim 16, wherein said DNA encodes an enzyme having the following physicochemical properties:
(1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
(2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.

18. The transformant as claimed in claim 16, wherein said DNA encodes an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

```
SEQ ID NO:2
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1               5                   10                  15
Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
        20                  25                  30
Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35                  40                  45                  50
Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
            55                  60                  65
```

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
70 75 80 85
Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
90 95 100
Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
105 110 115
Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
120 125 130 135
Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
140 145 150
Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
155 160 165 170
Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185
Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200
Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
205 210 215 220
Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235
Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285
Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
290 295 300 305
Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile

310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu

325 330 335 340

Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala

345 350 355

Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu

445 450 455

Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg

495 500 505 510

Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro

545 550 555 560

Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
565 570 575

Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
580 585 590 595

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
630 635 640 645

Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
685 690 695

Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
700 705 710

Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
715 720 725 730

Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
735 740 745

Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
750 755 760 765

Pro Ala Thr Gly Gly Lys Ser
770

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp

20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly

35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu

70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro

90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala

105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu

120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg

140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp

155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg

175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu

205 210 215 220

Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His

225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val

240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285

Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
290 295 300 305

Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340

Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
345 350 355

Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
360 365 370

Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
375 380 385 390

Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
395 400 405

Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
445 450 455

Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490

Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg

495 500 505 510

Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro

545 550 555 560

Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp

565 570 575

Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro

580 585 590 595

Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu

630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His

685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

700 705 710

Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr

715 720 725 730

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe

735 740 745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
770 775

19. The transformant as claimed in claim 16, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

SEQ ID NO:1

ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT 60
GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC 120
ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
GACCCGGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240
GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGCAG 300
AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360
GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480
CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540
TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600
GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660
GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720
GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780
CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840
GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900
CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960
GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080

ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140
ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200
CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
TTTCACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620
CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
CCGGACCCGG CATTCGAGGA GGCACTTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
GAGGTGCGTG CGGAACTTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TGCGTCCAAC 1800
TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860
ACCGAGTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GGCGCCCCTT CAGCTTCGCC 1920
GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TGCGGCGGAA CCGGCCCGAG 2040
CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100
TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
CAGTCGGGCG GCTGGCGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCCG 2280
GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

SEQ ID NO:3

ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC 60
GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360

GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540
TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600
GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660
GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC 720
GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780
CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900
CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200
CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620
CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740
GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920
GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040
CTGTTCACGG GGTACCGGCC GGTCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100

TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160

GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220

GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280

TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

20. The transformant as claimed in claim 19, wherein one or more bases in SEQ ID NOs:1 and 3 are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences as shown in the following SEQ ID NOs:2 and 4:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
155 160 165 170

Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200

Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
205 210 215 220

Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285

Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
290 295 300 305

Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340

Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
345 350 355

Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
360 365 370

Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
375 380 385 390

Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
395 400 405

Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu

445 450 455

Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg

495 500 505 510

Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro

545 550 555 560

Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp

565 570 575

Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro

580 585 590 595

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu

630 635 640 645

Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
685 690 695

Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
700 705 710

Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
715 720 725 730

Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
735 740 745

Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
750 755 760 765

Pro Ala Thr Gly Gly Lys Ser
770

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala

105 110 115
Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
120 125 130 135
Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
140 145 150
Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
155 160 165 170
Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185
Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200
Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
205 210 215 220
Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235
Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285
Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
290 295 300 305
Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
310 315 320
Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340
Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
345 350 355

Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
360 365 370
Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
375 380 385 390
Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
395 400 405
Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425
Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440
Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
445 450 455
Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490
Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
495 500 505 510
Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
515 520 525
Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
545 550 555 560
Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
565 570 575
Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
580 585 590 595
Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu

630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His

685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

700 705 710

Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr

715 720 725 730

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe

735 740 745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

770 775

21. The transformant as claimed in claim 16, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:10 and 11:

SEQ ID NO:10:

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60

CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120

GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180

CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240

TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300

GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360

GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420

GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA 480

CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540

AGGCAAGCAG GGCGGGACGG GCTC 564

ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
1 5 10 15

ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
20 25 30

GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
35 40 45

GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
50 55 60

GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
65 70 75 80

GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
85 90 95

TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
100 105 110

GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly

```
        115                 120                 125
GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG   996
Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
    130                 135                 140
CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG  1044
Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145                 150                 155                 160
CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC  1092
Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
                165                 170                 175
GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA  1140
Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
            180                 185                 190
CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG  1188
Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg
        195                 200                 205
GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC  1236
Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
    210                 215                 220
TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC  1284
Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
225                 230                 235                 240
GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC  1332
Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
                245                 250                 255
GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG  1380
Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
            260                 265                 270
TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC  1428
```

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu

275 280 285

GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476

Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu

290 295 300

GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524

Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu

305 310 315 320

GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572

Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His

325 330 335

TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620

Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile

340 345 350

CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668

Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe

355 360 365

CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716

Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu

370 375 380

GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764

Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val

385 390 395 400

CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812

Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg

405 410 415

AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860

Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp

420 425 430

ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
435 440 445

GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
450 455 460

ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465 470 475 480

ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
485 490 495

ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
500 505 510

ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
515 520 525

GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
530 535 540

GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
545 550 555 560

CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
565 570 575

TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu

580 585 590

CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln

595 600 605

CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp

610 615 620

GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala

625 630 635 640

GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532
Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp

645 650 655

TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580
Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu

660 665 670

CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628
Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val

675 680 685

CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676
His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly

690 695 700

GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724
Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu

705 710 715 720

CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772
Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met

725 730 735

ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820

Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
740 745 750

TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868
Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
755 760 765

GGA GGC AAG TCA 2880
Gly Gly Lys Ser
770

TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936

SEQ ID NO:11

GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60
GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240
TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT 300
CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420
GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480
GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
CCCGCTGGGG AGGACGC 677

ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
1 5 10 15

ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773
Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
20 25 30

GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821
Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
35 40 45

GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
50 55 60

GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
65 70 75 80

GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
85 90 95

ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
100 105 110

CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
115 120 125

GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
130 135 140

CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145 150 155 160

CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
165 170 175

GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu

180 185 190

CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301

Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg

195 200 205

GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349

Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg

210 215 220

TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397

Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp

225 230 235 240

GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445

Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr

245 250 255

GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493

Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC 1541

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu

275 280 285

GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589

Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu

290 295 300

GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637

Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln

305 310 315 320

GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685

Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His

325 330 335

TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733

Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
340 345 350

TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781
Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
355 360 365

CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
370 375 380

GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
385 390 395 400

CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
405 410 415

CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
420 425 430

ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
435 440 445

GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
450 455 460

CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465 470 475 480

ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
485 490 495

ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
500 505 510

GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
515 520 525

GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540

GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
545 550 555 560

CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
565 570 575

TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
580 585 590

CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG 2501
Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
595 600 605

CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
610 615 620

GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
625 630 635 640

GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala

```
                  645                 650                 655
TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG  2693
Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
              660                 665                 670
CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC  2741
Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
          675                 680                 685
CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC  2789
Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
      690                 695                 700
ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC  2837
Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
705                 710                 715                 720
GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC  2885
Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
                  725                 730                 735
ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA  2933
Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
              740                 745                 750
GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG  2981
Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
          755                 760                 765
CCG CAG ACA GGA GGA GAG TCA                                      3002
Pro Gln Thr Gly Gly Glu Ser
      770                 775
TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
TCTGGGCGCC C                                                      3073
```

22. The transformant as claimed in claim 16, wherein said DNA is derived from a microorganism selected from the group consisting of the genera *Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium* and *Terrabacter*.

23. The transformant as claimed in claim 16, wherein said self-replicable vector is a plasmid vector Bluescript II SK(+).

24. The transformant as claimed in claim 16, wherein said host is a microorganism of the spices *Escherichia coli.*

25. A recombinant enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.

26. The recombinant enzyme as claimed in claim 25, which has the following physicochemical properties:
(1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
(2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.

27. The recombinant enzyme as claimed in claim 25, which has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

```
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1               5                   10                  15
Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
```

20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly

35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu

70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro

90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala

105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu

120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg

140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp

155 160 165 170

Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg

175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

190 195 200

Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu

205 210 215 220

Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His

225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val

240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285
Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
290 295 300 305
Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
310 315 320
Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340
Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
345 350 355
Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
360 365 370
Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
375 380 385 390
Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
395 400 405
Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425
Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440
Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
445 450 455
Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490
Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
495 500 505 510
Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro

545 550 555 560

Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp

565 570 575

Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro

580 585 590 595

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu

630 635 640 645

Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His

685 690 695

Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg

700 705 710

Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu

715 720 725 730

Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly

735 740 745

Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val

750 755 760 765

Pro Ala Thr Gly Gly Lys Ser

770

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu

205 210 215 220

Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His

225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val

240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala

275 280 285

Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg

290 295 300 305

Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile

310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu

325 330 335 340

Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly

345 350 355

Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp

445 450 455

Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
480 485 490

Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
495 500 505 510

Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
545 550 555 560

Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
565 570 575

Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
580 585 590 595

Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

```
            700                      705                      710
Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
715                     720                      725                      730
Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
                735                      740                      745
Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
    750                      755                      760                      765
Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
                        770                      775
```

28. A process for producing a recombinant enzyme, which comprises culturing a transformant capable of forming the recombinant enzyme of claim 25, and collecting the recombinant enzyme from the resultant culture.

29. The process as claimed in claim 28, wherein said recombinant enzyme has the following physicochemical properties:
(1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
(2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.

30. The process of as claimed in claim 28, wherein said recombinant enzyme has an amino acid sequence selected from the group consisting of those as shown in SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

```
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1               5                   10                  15
```

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly

35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu

70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro

90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala

105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu

120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg

140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp

155 160 165 170

Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg

175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

190 195 200

Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu

205 210 215 220

Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His

225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val

240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala

275 280 285

Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg

290 295 300 305

Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile

310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu

325 330 335 340

Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala

345 350 355

Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu

445 450 455

Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg

495 500 505 510

Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
545 550 555 560

Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
565 570 575

Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
580 585 590 595

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
630 635 640 645

Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
685 690 695

Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
700 705 710

Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
715 720 725 730

Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
735 740 745

Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val

750 755 760 765

Pro Ala Thr Gly Gly Lys Ser

770

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
205 210 215 220
Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235
Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285
Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
290 295 300 305
Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
310 315 320
Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340
Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
345 350 355
Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
360 365 370
Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
375 380 385 390
Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
395 400 405
Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425
Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440
Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp

```
        445                 450                 455
Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460                 465                 470                 475
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
            480                 485                 490
Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
    495                 500                 505                 510
Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
                515                 520                 525
Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
        530                 535                 540
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
545                 550                 555                 560
Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
            565                 570                 575
Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
    580                 585                 590                 595
Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
                600                 605                 610
Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
        615                 620                 625
Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
630                 635                 640                 645
Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
            650                 655                 660
Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
    665                 670                 675                 680
Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
                685                 690                 695
```

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
700 705 710
Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
715 720 725 730
Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
735 740 745
Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
750 755 760 765
Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
770 775

31. The process as claimed in claim 28, wherein said transformant is obtained by introducing into a suitable host a recombinant DNA containing a self-replicable vector and a DNA encoding an enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.

32. The process as claimed in claim 28, wherein said DNA has a base sequence selected from the group consisting of those as shown in SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequence to these base sequences:

SEQ ID NO:1
ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT 60
GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC 120
ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
GACCCGGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240
GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGCAG 300
AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360

GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480
CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540
TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600
GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660
GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720
GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780
CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840
GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900
CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960
GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140
ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200
CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
TTTCACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620
CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
CCGGACCCGG CATTCGAGGA GGCACTTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
GAGGTGCGTG CGGAACTTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TGCGTCCAAC 1800
TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860
ACCGAGTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GGCGCCCCTT CAGCTTCGCC 1920
GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TGCGGCGGAA CCGGCCCGAG 2040
CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100

TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
CAGTCGGGCG GCTGGCGGGA CACCGC[illegible]GTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCCG 2280
GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

SEQ ID NO:3

ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC 60
GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540
TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600
GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660
GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC 720
GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780
CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900
CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080
CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200
CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380

```
TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620
CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740
GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860
ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920
GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040
CTGTTCACGG GGTACCGGCC GGTCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220
GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA                2325
```

33. The process as claimed in claim 32, wherein said DNA has a base sequence selected from the group consisting of those as shown in SEQ ID NOs:1 and 3 wherein one or more bases are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences as shown in the following SEQ ID NOs:2 and 4:

SEQ ID NO:2

```
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1               5                   10                  15
Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
        20                  25                  30
Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35                  40                  45                  50
```

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
155 160 165 170

Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200

Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
205 210 215 220

Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285

Asp val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg

290 295 300 305

Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile

310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu

325 330 335 340

Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala

345 350 355

Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu

445 450 455

Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg

495 500 505 510

Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
545 550 555 560

Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
565 570 575

Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
580 585 590 595

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
630 635 640 645

Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
685 690 695

Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
700 705 710

Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
715 720 725 730

Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
735 740 745

Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
750 755 760 765

Pro Ala Thr Gly Gly Lys Ser
770

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
205 210 215 220

Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255
Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285
Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
290 295 300 305
Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
310 315 320
Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340
Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
345 350 355
Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
360 365 370
Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
375 380 385 390
Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
395 400 405
Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425
Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440
Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
445 450 455
Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475
Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg

495 500 505 510

Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro

545 550 555 560

Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp

565 570 575

Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro

580 585 590 595

Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu

630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His

685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

700 705 710

Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr

715 720 725 730

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Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
            735                     740                     745
Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
    750                     755                     760                     765
Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
                770                     775
```

34. The process as claimed in claim 28, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:10 and 11:

SEQ ID NO:10:

```
CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA  60
CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT  120
GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG  180
CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC  240
TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA  300
GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA  360
GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC  420
GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA  480
CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC  540
AGGCAAGCAG GGCGGGACGG GCTC                                          564
ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC     612
Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
1               5                   10                  15
ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG     660
Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
            20                  25                  30
GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC     708
Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
        35                  40                  45
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GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
50 55 60

GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
65 70 75 80

GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
85 90 95

TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
100 105 110

GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
115 120 125

GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
130 135 140

CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044
Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145 150 155 160

CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092
Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
165 170 175

GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140
Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
180 185 190

CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188
Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg

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        195                 200                 205
GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC   1236
Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
    210                 215                 220
TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC   1284
Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
225                 230                 235                 240
GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC   1332
Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
                245                 250                 255
GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG   1380
Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
            260                 265                 270
TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC   1428
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
        275                 280                 285
GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG   1476
Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
    290                 295                 300
GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG   1524
Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
305                 310                 315                 320
GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC   1572
Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                325                 330                 335
TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT   1620
Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
            340                 345                 350
CCC GCG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC   1668
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Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
355 360 365

CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
370 375 380

GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
385 390 395 400

CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
405 410 415

AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
420 425 430

ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
435 440 445

GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
450 455 460

ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465 470 475 480

ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
485 490 495

ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
500 505 510

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ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG   2148
Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
        515                 520                 525
GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC   2196
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
    530                 535                 540
GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT   2244
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
545                 550                 555                 560
CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC   2292
Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
                565                 570                 575
TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC   2340
Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
            580                 585                 590
CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG   2388
Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
        595                 600                 605
CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG   2436
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
    610                 615                 620
GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC   2484
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
625                 630                 635                 640
GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC   2532
Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
                645                 650                 655
TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG   2580
Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
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                660                     665                     670
CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG   2628
Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
            675                     680                     685
CAT GCC AGG GGC CCC GCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC   2676
His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
        690                     695                     700
GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA   2724
Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
705                     710                     715                     720
CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG   2772
Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
                    725                     730                     735
ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG   2820
Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
                740                     745                     750
TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA   2868
Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
            755                     760                     765
GGA GGC AAG TCA                                                   2880
Gly Gly Lys Ser
        770
TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC     2936
```

SEQ ID NO:11

```
GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG  60
GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240
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TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT 300
CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420
GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480
GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
CCCGCTGGGG AGGACGC 677

ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
1 5 10 15

ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773
Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
20 25 30

GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821
Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
35 40 45

GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
50 55 60

GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
65 70 75 80

GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
85 90 95

ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
100 105 110

CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
115 120 125

GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
130 135 140

CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
145 150 155 160

CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
165 170 175

GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
180 185 190

CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg
195 200 205

GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349
Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
210 215 220

TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397
Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
225 230 235 240

GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445
Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
245 250 255

GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493
Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

```
            260                 265                 270
CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC   1541
Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
        275                 280                 285
GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG   1589
Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu
    290                 295                 300
GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG   1637
Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln
305                 310                 315                 320
GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC   1685
Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                325                 330                 335
TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT   1733
Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
            340                 345                 350
TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC   1781
Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
        355                 360                 365
CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG   1829
Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
    370                 375                 380
GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC   1877
Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
385                 390                 395                 400
CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG   1925
Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
                405                 410                 415
CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC   1973
```

Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
420 425 430

ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
435 440 445

GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
450 455 460

CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
465 470 475 480

ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
485 490 495

ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
500 505 510

GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
515 520 525

GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
530 535 540

GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
545 550 555 560

CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
565 570 575

```
TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC   2453
Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
            580                 585                 590
CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG   2501
Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
        595                 600                 605
CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG   2549
Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
    610                 615                 620
GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC   2597
Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
625                 630                 635                 640
GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG   2645
Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
                645                 650                 655
TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG   2693
Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
            660                 665                 670
CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC   2741
Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
        675                 680                 685
CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC   2789
Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
    690                 695                 700
ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC   2837
Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
705                 710                 715                 720
GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC   2885
Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
```

```
                 725                        730                        735
ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA   2933
Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
             740                        745                        750
GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG   2981
Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
         755                        760                        765
CCG CAG ACA GGA GGA GAG TCA                                        3002
Pro Gln Thr Gly Gly Glu Ser
     770                        775
TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
TCTGGGCGCC C                                                       3073
```

35. The process as claimed in 28, wherein said DNA is derived from a microorganism selected from the group consisting of the genera *Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium* and *Terrabacter.*

36. The process as claimed in claim 28, wherein said host is a microorganism of the spices *Escherichia coli.*

37. The process as claimed in claim 28, wherein said self-replicable vector is plasmid vector Bluescript II SK(+).

38. The process as claimed in claim 28, wherein said transformant is inoculated into a liquid culture medium having a pH of 2-8, and cultured at a temperature of 25-65°C for 1-6 days.

39. The process as claimed in claim 28, wherein said recombinant enzyme in the culture is collected by one or more methods selected from the group consisting of centrifugation, filtration, concentration, salting out, dialysis, ion-exchange chromatography, gel filtration chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectrophoresis.

40. A method to convert a reducing amylaceous saccharide, which contains a step of allowing the recombinant enzyme of claim 25 to act on a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher to form a non-reducing saccharide having trehalose structure as an end unit from the amylaceous saccharide.

41. The method as claimed in claim 40, wherein said recombinant enzyme has the following physicochemical properties:

(1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
(2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.

42. The method as claimed in claim 40, wherein said recombinant enzyme has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1 5 10 15
Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
20 25 30
Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
155 160 165 170

Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200

Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
205 210 215 220

Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285

Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg

290 295 300 305

Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile

310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu

325 330 335 340

Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala

345 350 355

Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr

360 365 370

Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg

375 380 385 390

Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu

395 400 405

Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val

410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu

445 450 455

Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met

460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg

495 500 505 510

Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr

530 535 540

```
Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
545                 550                 555                 560
Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
            565                 570                 575
Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
    580                 585                 590                 595
His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
                600                 605                 610
Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
        615                 620                 625
Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
630                 635                 640                 645
Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
            650                 655                 660
Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
    665                 670                 675                 680
Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
                685                 690                 695
Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
        700                 705                 710
Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
715                 720                 725                 730
Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
            735                 740                 745
Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
    750                 755                 760                 765
Pro Ala Thr Gly Gly Lys Ser
                770
```

SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
205 210 215 220

Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
225 230 235

Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
240 245 250 255

Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
275 280 285

Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
290 295 300 305

Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
310 315 320

Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
325 330 335 340

Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
345 350 355

Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
360 365 370

Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
375 380 385 390

Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
395 400 405

Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
410 415 420 425

Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
430 435 440

Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
445 450 455

Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
460 465 470 475

Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

480 485 490

Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg

495 500 505 510

Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp

515 520 525

Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr

530 535 540

Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro

545 550 555 560

Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp

565 570 575

Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro

580 585 590 595

Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

600 605 610

Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu

630 635 640 645

Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr

650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu

665 670 675 680

Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His

685 690 695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

700 705 710

Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr

715 720 725 730

```
Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
                735                 740                 745
Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
    750                 755                 760                 765
Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
                770                 775
```

43. The method as claimed in claim 40, wherein said reducing amylaceous saccharide is a member selected from the group consisting of starch hydrolysate and amylaceous substance which has been treated with acid together with or without amylase.

44. The method as claimed in claim 40, wherein said reducing amylaceous saccharide is a member selected from the group consisting of maltotriose, maltotetraose, maltopentaose, maltohexaose, maltoheptaose and mixtures thereof.

45. The method as claimed in claim 40, wherein the reducing amylaceous saccharide is in a solution form with a concentration of 50 w/v % or lower, and the step is carried out at a temperature of 40-55°C and a pH of 5-10.

46. The method as claimed in claim 40, wherein said non-reducing saccharide is a member selected from the group of consisting of α-glucosyl trehalose, α-maltosyl trehalose, α-maltotriosyl trehalose, α-maltotetraosyl trehalose, α-maltopentaosyl trehalose, and mixtures thereof.

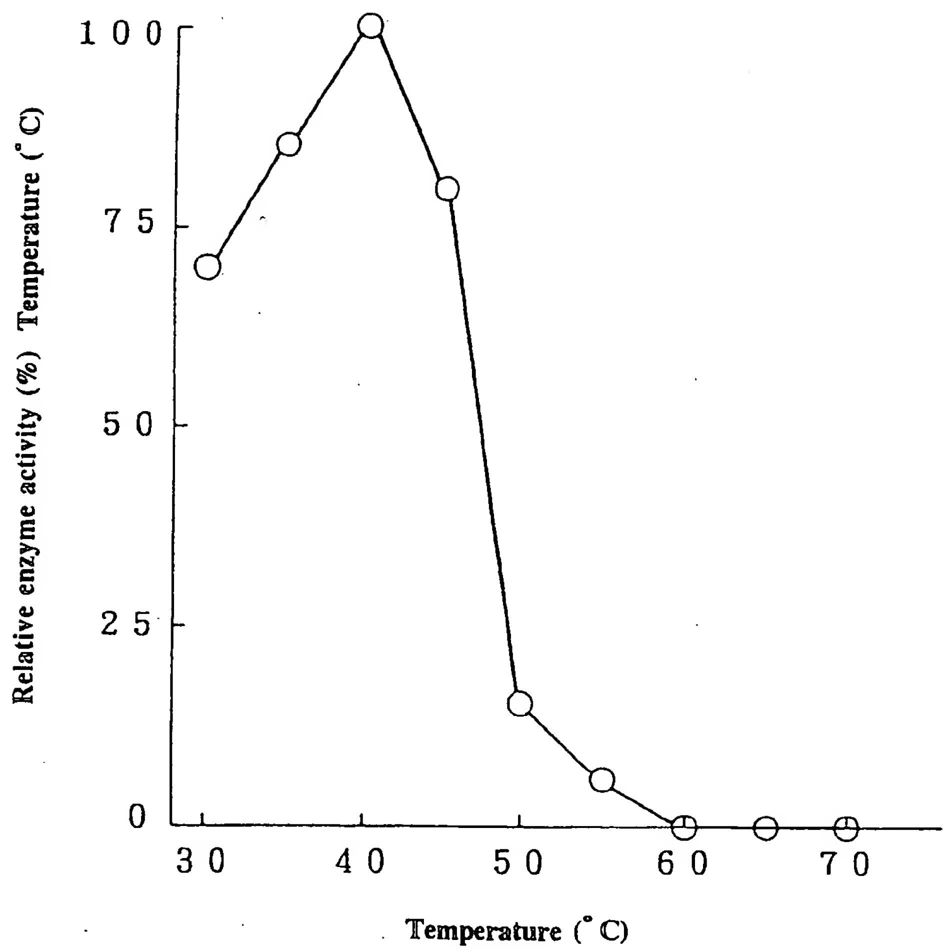

100
75
50
25
0
Relative enzyme activity (%) Temperature (°C)
30
40
50
60
70
Temperature (°C)

FIG. 1

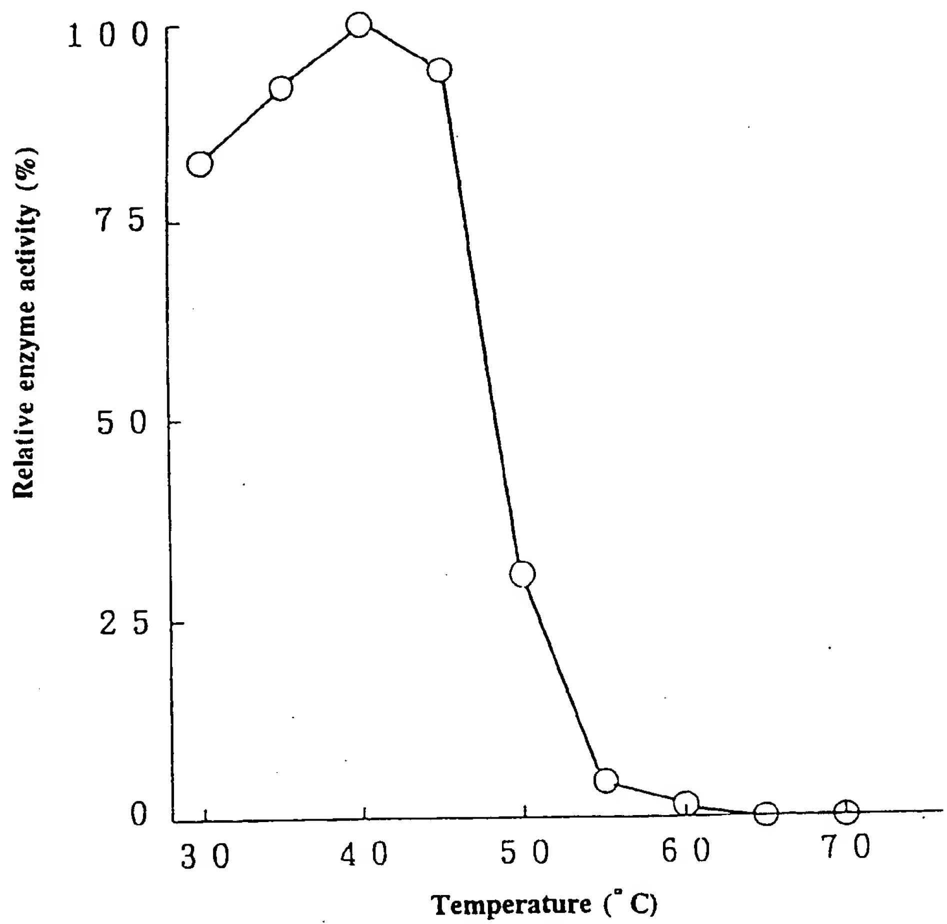

1 0 0
7 5
5 0
2 5
0
Relative enzyme activity (%)
3 0
4 0
5 0
6 0
7 0
Temperature (° C)

FIG. 2

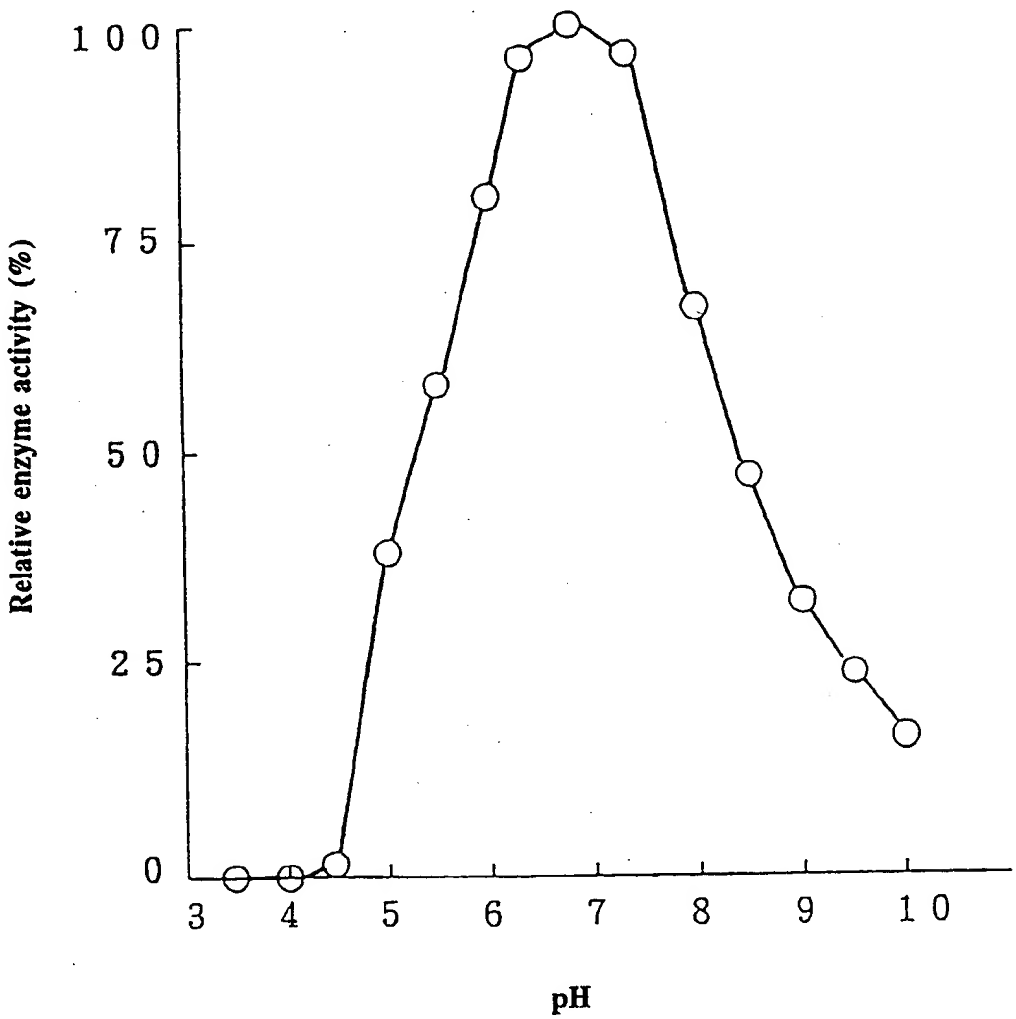


FIG. 3

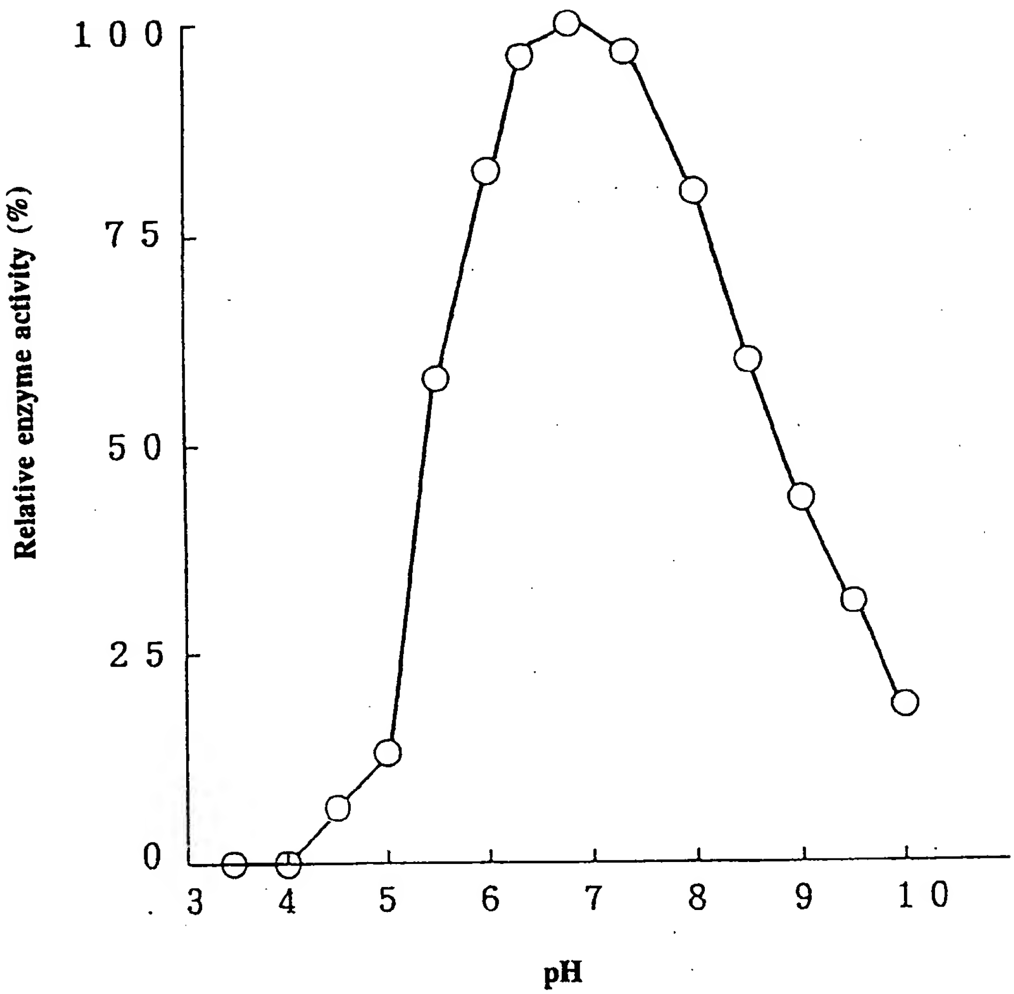


FIG. 4

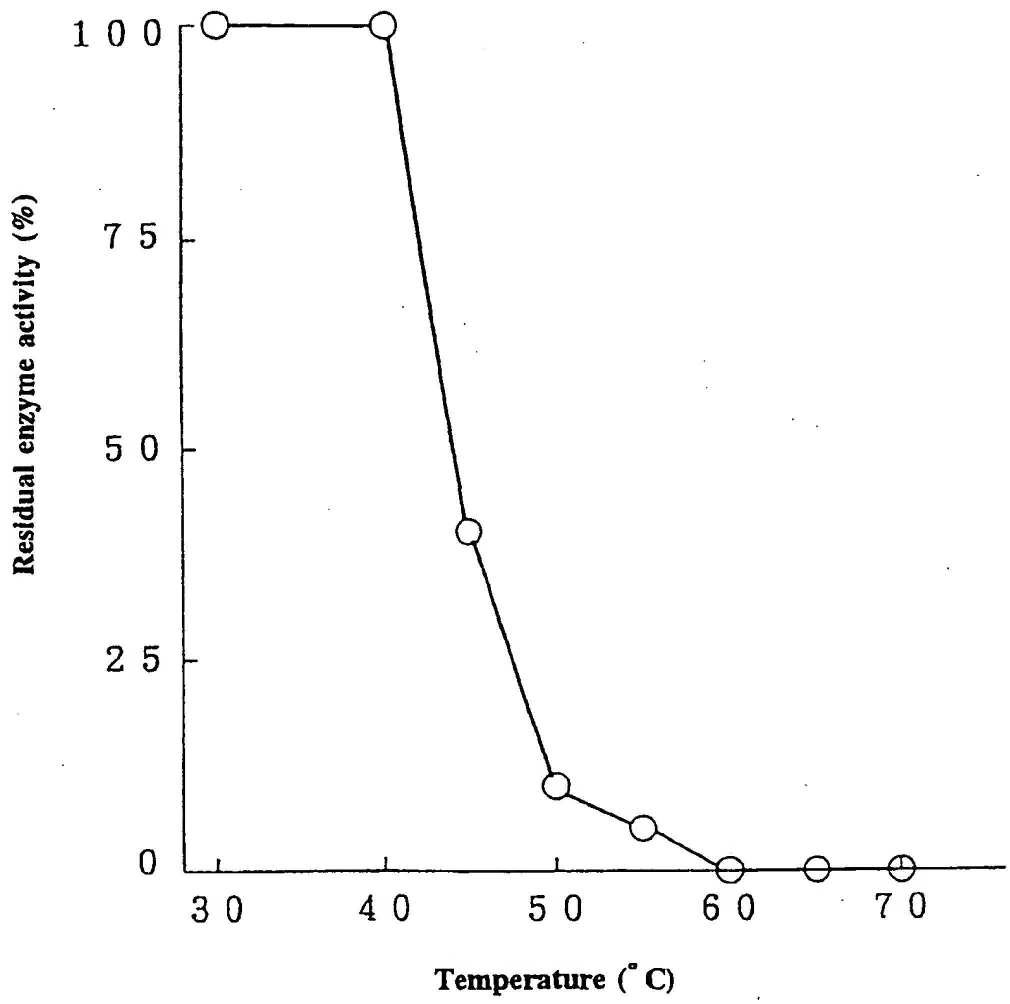
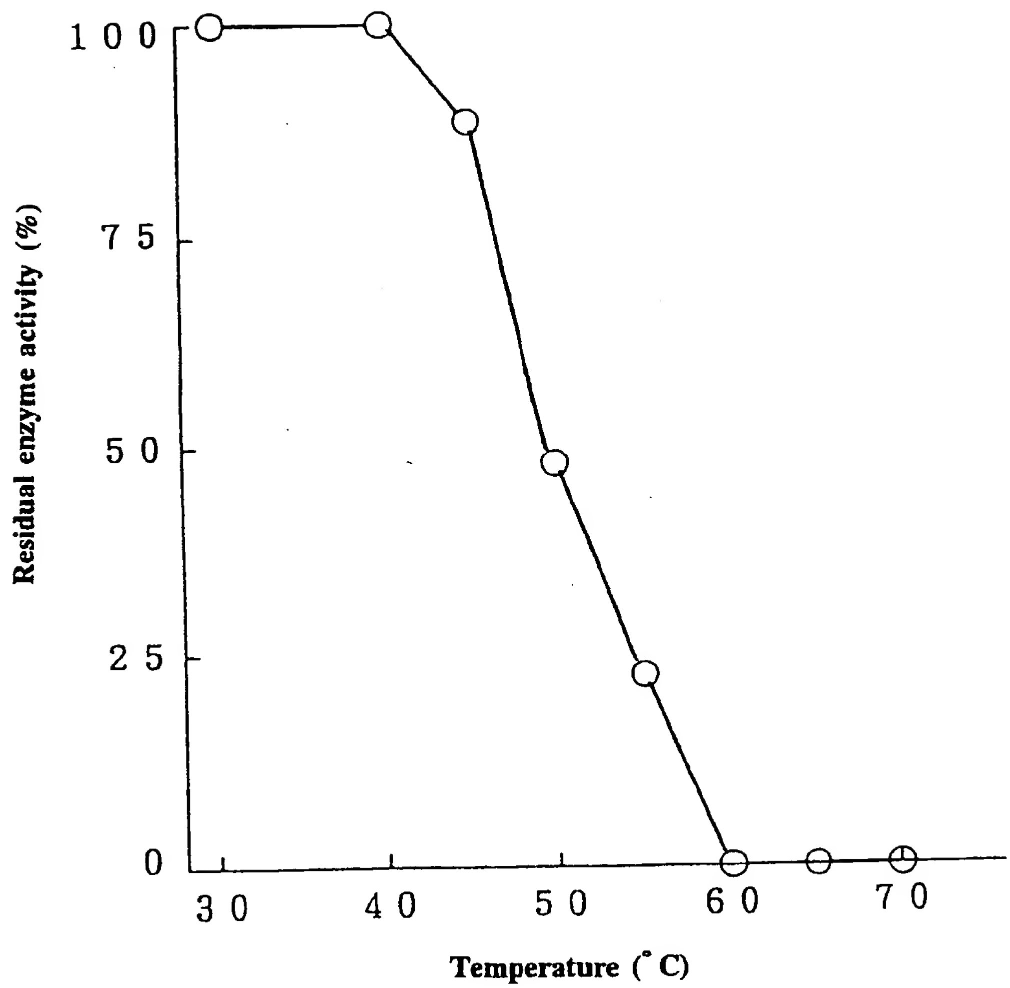

100
75
50
25
0
30
40
50
60
70
Residual enzyme activity (%)
Temperature (°C)

FIG. 5



100
75
50
25
0
Residual enzyme activity (%)
30
40
50
60
70
Temperature (° C)

FIG. 6

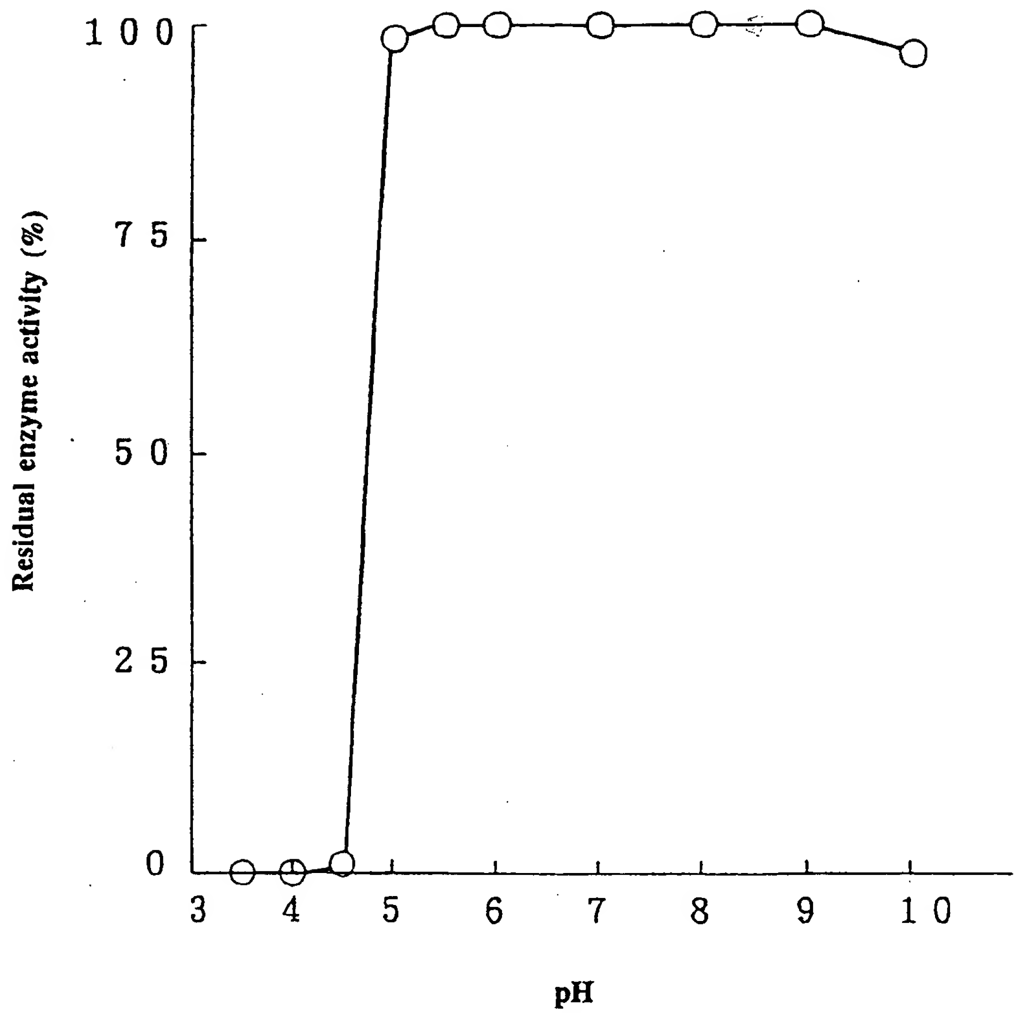


FIG. 7

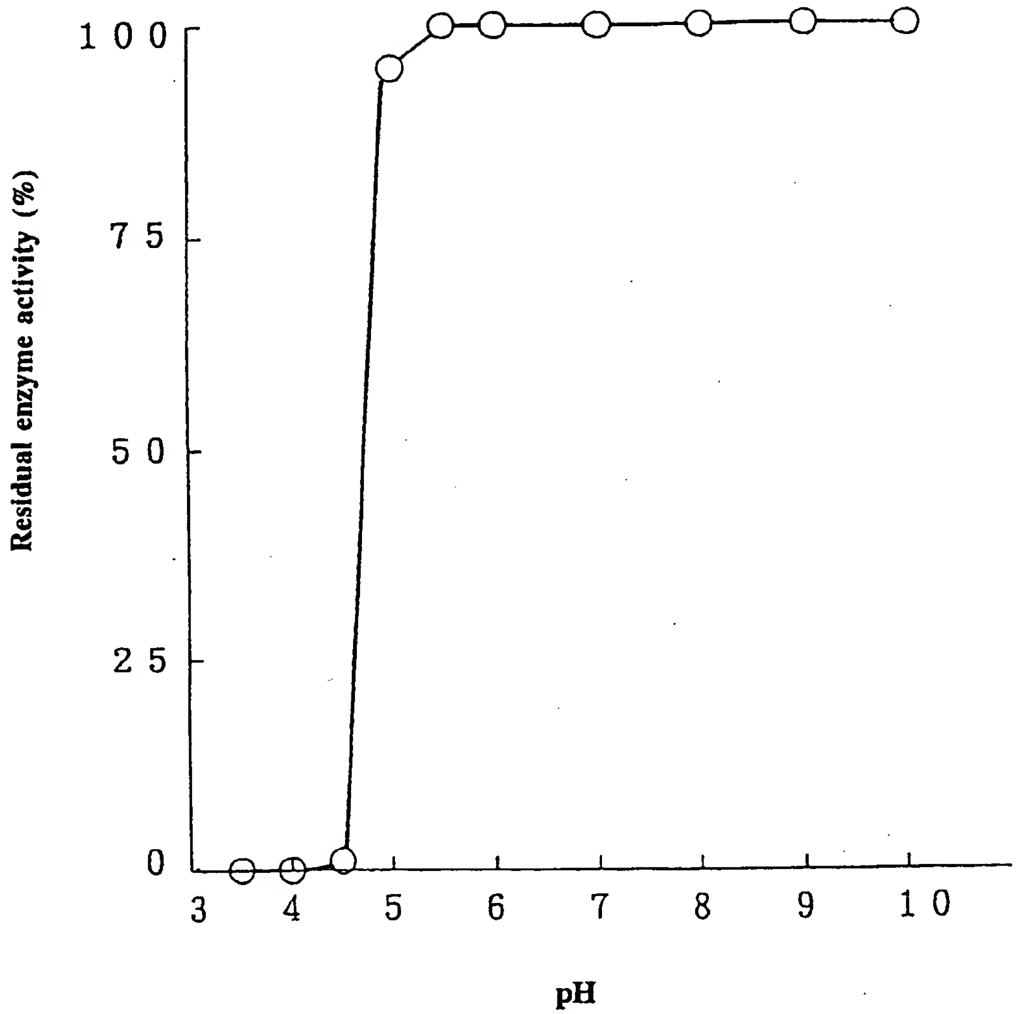


FIG. 8

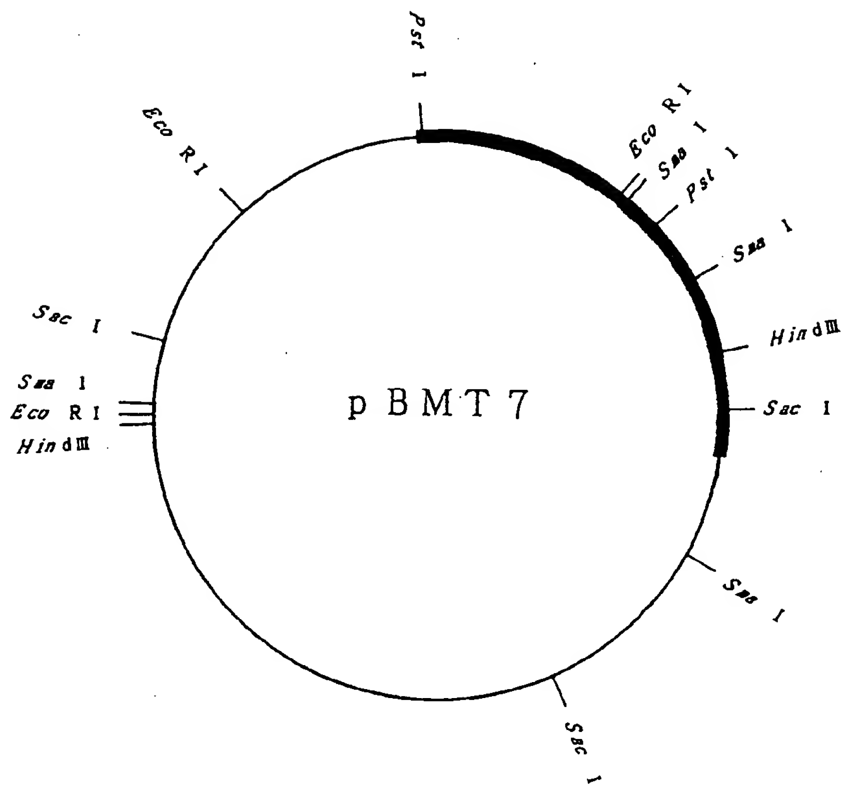

pBMT7
Pst I
Eco RI
Sma I
Pst I
Sma I
HindIII
Sac I
Sma I
Sac I
Eco RI
Sac I
Sma I
Eco RI
HindIII

FIG. 9

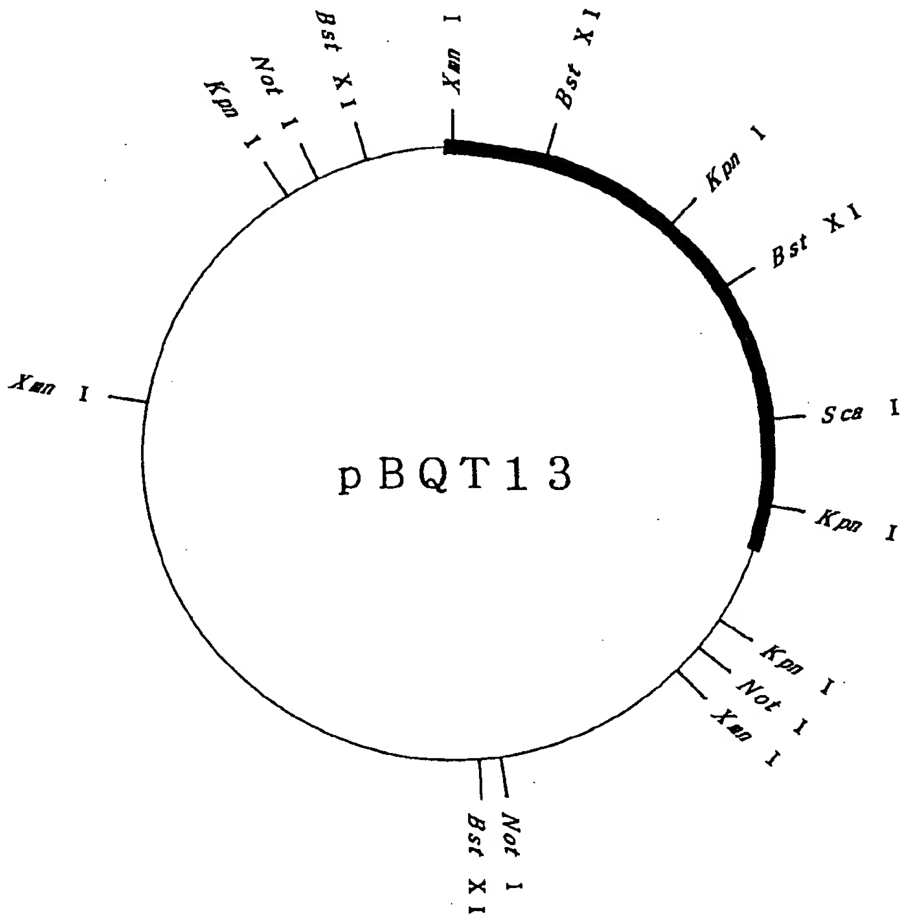

Xmn I
Bst X I
Kpn I
Bst X I
Sca I
Kpn I
Kpn I
Not I
Xmn I
Not I
Bst X I
Xmn I
Kpn I
Not I
Bst X I
pBQT13

FIG. 10